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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 23:41:33 / Search time 5120.53 seconds
(without alignments)
10809.568 Million cell updates/sec

Title: US-09-692-077D-1

Perfect score: 1353

Sequence: 1 atgacacacagaccctca.....ggaccagagcgctcgtca 1353

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size: 30

Total number of hits satisfying chosen parameters: 1678

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: GenEmbl:

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41: em_hcg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353	100.0	1353	6 AX350489	AX350489 Sequence
2	1353	100.0	9842	6 AF005900	AF005900 Homo sapi
3	1251	92.5	2072	6 AR270618	AR270618 Sequence
4	1251	92.5	2072	6 AR270618	AR270618 Sequence
5	1251	92.5	2072	6 AR270618	AR270618 Sequence
6	902	66.7	1344	6 AX350490	AX350490 Sequence
7	902	66.7	1344	6 AX350490	AX350490 Sequence
8	902	66.7	1344	6 AX350490	AX350490 Sequence
9	819	60.5	885	9 HUMA2C2	AC092603 Homo sapi
10	516	38.1	1030	9 HSA325747	M38742 Human alpha
11	463	34.2	828	10 S67316	AJ325747 Homo sapi
12	230	17.0	249	10 S67320	S67316 alpha 2-adr
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14	137	10.1	1150	4 CS2251181	AJ251181 Cynopteri
15	132	9.8	246	10 S6731782	S67319 alpha 2-adr
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18	116	8.6	1168	4 TTA251187	AJ251187 Tupia ta
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ALIGNMENTS

RESULT 1
AX350489
LOCUS AX350489 1353 bp DNA
DEFINITION Sequence 1 from Patent WO0179561.
ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 1 25-OCT-2001;

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BASE COUNT      224 a      458 c      405 g      266 t
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QY	61	TTCTCATTTCTTTACCATTTTCGACAGCTCTGGTCAATCCGTGCTGTGTGACGAG	120
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QY	421	GCGGTATCTGCTGCGCGCCCTCATCTCAAGAGGAGCCAGGGGCCCCAGCGCGCGCGG	480
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RESULT 2				
AFO05900				
LOCUS	AF005900	9642 bp	DNA	linear PRI 08-JUL-1997
DEFINITION	Homo sapiens alpha2B-adrenergic receptor (alpha2CZAR) gene,			
ACCESSION	AF005900			
VERSION				
KEYWORDS	AF005900.1 GI:2245627			
SOURCE				
ORGANISM				
REFERENCE	Homo sapiens (human)			
TITLE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 9842)			
TITLE	Cayla,C., SchaaK,S., Bouloumie,A., Dovedjian,J.C. and Paris,H.			
REFERENCE	Alpha2C2-adrenergic receptor gene			
TITLE	Unpublished			
REFERENCE	2 (bases 1 to 9842)			
TITLE	Cayla,C., Schaak,S., Bouloumie,A., Dovedjian,J.C. and Paris,H.			
REFERENCE	Direct Submission			
TITLE	Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,			
JOURNAL	CHU Rangueil, Toulouse 31403, France			
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 5458 TTCCTCATTTCTTTACCATCTTTCGGCAAGCTCTGTATCTGTGCTGTGTGACAC 5517
QY 121 CGCTGCTGCGGCGCCCTGAGAACCTGTTCTGTGTGCTGCTGCGCGCGCAATCTG 180
DB 5518 CGCTGCTGCGGCGCCCTGAGAACCTGTTCTGTGTGCTGCTGCGCGCGCAATCTG 5577
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QY 241 CGGCGCAGTGTGCGAGGTGTACTGTGCGCTGAGCTGTCTTCTGACCTGTCTATC 300
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RESULT 3
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LOCUS AR270618 2072 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1181 from patent US 650938.
ACCESSION AR270618
VERSION AR270618.1 GI:29701852
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2072)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 650938-A 1181 31-DEC-2002;
FEATURES
location/Qualifiers
source
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BASE COUNT 316 a 705 c 660 g 391 t
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 473 TTCCTCATTTCTTTACCATCTTTCGGCAAGCTCTGTATCTGTGCTGTGTGACAC 532
QY 121 CGCTGCTGCGGCGCCCTGAGAACCTGTTCTGTGTGCTGCTGCGCGCGCAATCTG 180
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OY	301	GTGCACTGTGTGAGAGTGTACTTGGCCGCTCGACGTGCTCTTCTGCACTCTGTCCATC	360
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COMMENT	FEATURES	source
Original source text: Human placenta DNA, clone alpha-2 C2. Draft entry and computer-readable sequence for [1] kindly submitted by J.W. Lomareney, 03-MAY-1990, for release after publication.	Location/Qualifiers 1..2072	gene
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BASE COUNT	316 a 705 c 660 g 391 t	
ORIGIN	Chromosome 2.	
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Best Local Similarity	99.9%: Pred. No. 0;	
Matches 1351; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
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DB	 413 ATGAGCACACGAGACCCCTACTCCGTGTCAGGACCCACAGCGCCCATAGCGGCGCCATACCC 472	
QY	61 TTCCCATATTCCTTTACCATCATCTTGCGGACAGCGCTCGGTCATCCGTGGCTGTGTGACGACG 120	
DB	 473 TTCCCATATTCCTTTACCATCATCTTGCGGACAGCGCTCGGTCATCCGTGGCTGTGTGACGACG 532	
QY	121 CGCTGCTGCGGCGCCCTCAGAAACTGTCTTCGTGTGTGCTGTGCGCGCGCGACATCTCTG 180	
DB	533 CGCTGCTGCGGCGCCCTCAGAAACTGTCTTCGTGTGTGTGCTGTGCGCGCGCGACATCTCTG 592	

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241 CGGCGCAGCTGTGGGAGGTGTAAGTGGGCTGTGAGCTGTCTTCTGCACTGTCCATC 300
653 CGGCGCAGCTGTGGGAGGTGTAAGTGGGCTGTGAGCTGTCTTCTGCACTGTCCATC 712
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DB 1733 CTGTGCGGCGCGTGAACCGAGCGGCTGTGA 1765
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LOCUS AX548756 3274 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 41 from Patent WO02061087.
ACCESSION AX548756
VERSION AX548756.1 GI:25813686
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Burnier, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 41 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 6
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LOCUS AX350490 Sequence 2 from Patent WO0179561.
DEFINITION AX350490
ACCESSION AX350490
VERSION AX350490.1 GI:18616092
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Liggett, S.B. and Small, K.M.
Alpha-2 adrenergic receptor polymorphisms

JOURNAL Patent: WO 0179561-A 2 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
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REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 22842)
TITLE Sulston, J.E. and Waterston, R.
JOURNAL Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074

REFERENCE 2 (bases 1 to 22842)
AUTHORS Martinik, S., Abbott, A., Hawkins, M., Elliott, G. and Doeber, A.
TITLE The sequence of Homo sapiens BAC clone Rpl1-13956
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 22842)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 22842)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 22842)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 22842)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 20, 2001 this sequence version replaced gi:14916188.

COMMENT ----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUSC
Web site: <http://genome.wustl.edu/gsc>
Contact: saplens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH013906
Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30) ; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPl1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tatem, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBac3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
The clone sequenced to the right is RP11-574O17, 2000 bp overlap.
The clone sequenced to the right is RP11-574O17, 2000 bp overlap.
Actual end of this clone is at base position 48999 of RP11-574O17
Polymorphisms have been identified between AC013272 and AC0592603.

The sequence of AC073396 has been incorporated into AC092603.

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QY	901	GA 902	
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HMA2C2	RESULT 9
LOCUS	HUMA2C2 885 bp DNA linear PRI 06-MAR-1995
DEFINITION	Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cds.
ACCESSION	M38742
VERSION	M38742.1 GI:177867
KEYWORDS	alpha-2 adrenergic receptor.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 885) Chang,A.C., Ho,T.F. and Chang,N.C. In vitro amplification by polymerase chain reaction of a partial gene encoding the third subtype of alpha-2 adrenergic receptor in humans Biochem. Biophys. Res. Commun. 172 (2), 817-823 (1990)
JOURNAL MEDLINE PubMed	91054503 2173582
COMMENT	Original source text: Human adult neuroblastoma DNA, clone PCRA2. Diff entry and computer-readable sequence for [unpublished (1990)] kindly submitted by A.C.Chang, 20-SEP-1990. Institute of Neuroscience 155, Sect II, Li-Neon St. Taipei, Taiwan, 11221 ROC.
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Db	208	GCATTTCCAGAGAGTAAGAGCTGMAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT	149
Oy	921	GAACCCAGGAGAGTAGTCACAGTGTCTCCGGGCTCAGCTTCAGCCCCCGCTGCAGACGCA	990
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Oy	991	CAGGCTCCCGGAGTGCCTGCCACCTTACGTGGCCAGTGTCTCTTGGGAGAGGAGCGTGGGT	1050
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Oy	1051	GCTATAGGTGGGCACTGTGGCGTTCGA	1077
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RESULT	11		
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DEFINITION	alpha 2-adrenergic receptor [rats; Sprague-Dawley, islets of Langerhans, mRNA Partial, 828 nt].		
VERSION	S67316		
KEYWORDS	S67316.1 GI:456949		
SOURCE	Rattus sp.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.		
REFERENCE	Wang,S.Y. and Pilkey,D.T. Identification in islets of Langerhans of a new rat alpha 2-adrenergic receptor Diabetes 43 (1), 127-136 (1994)		
JOURNAL MEDLINE	GenBank staff at the National Library of Medicine created this entry [NCBI glibedg 140730] from the original journal article.		
PUBMED	94085695		
REMARK	This sequence comes from fig. 1.		
FEATURES	Location/Qualifiers		
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BASE COUNT	148 a 271 c 269 g 140 t		
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Query Match	34.2%; Score 463; DB 10; Length 828;		
Best Local Similarity	99.6%; Pred. No. 1,2e-225;		
Matches	563; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
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Oy	367	AAGGCAACCCCGCGCGCATCAAGTGCATCATCTGCTATGTGGCTATATGCCGCGTCC	426

Db	82	AAGCGCACCCGCGCGCGCATCAAGTGCATCATCTCACTGTTGGCTCATTCGCGCGCTC	141
Oy	427	ATTCGCTGCGCGCCCTCATCTCAACAAGGGCGACCAAGGGCCCCCAAGCGCGCGCGCGCC	486
Db	142	ATTCGCTGCGCGCCCTCATCTCAACAAGGGCGACCAAGGGCCCCCAAGCGCGCGCGCC	201
Oy	487	CAGTCAAGCTCAACCAAGAGGGCTGGTACATCTGGCTCCAGCATCGGATCTTCTT	548
Db	202	CAGTCAAGCTCAACCAAGAGGGCTGGTACATCTGGCTCCAGCATCGGATCTTCTT	261
Oy	547	GCTCCTTGCCCTCATCATGATCCTTGTCTTAACTCGGCGATCTACTGATTCGCCAAAGCAGC	606
Db	262	GCTCCTTGCCCTCATCATGATCCTTGTCTTAACTCGGCGATCTACTGATTCGCCAAAGCAGC	321
Oy	607	AACGCGAAGGTCCTCCAGGGCCCAAGGGGGGCTTGGGCAAGGTGAGTCCAAAGCAGCCCGA	666
Db	322	AACGCGAAGGTCCTCCAGGGCCCAAGGGGGGCTTGGGCAAGGTGAGTCCAAAGCAGCCCGA	381
Oy	667	CCCCACCATGTGTGGGGCTTTGGCTCTCAAGCCAACTGCGAGCCCTTGCTGTGGCTTCT	726
Db	382	CCCCACCATGTGTGGGGCTTTGGCTCTCAAGCCAACTGCGAGCCCTTGCTGTGGCTTCT	441
Oy	727	GCCAGAGAGTCTCAACGGAACCTCGAAGTCCACTGGGAGAAAGAGAGGGGAGACCCCT	786
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Oy	787	GAAGATCTGGGACCCCGGCTTGGCCACCCAGTTGGGCTGCCCTTCCCACTCAGGCGAG	846
Db	502	GAAGATCTGGGACCCCGGCTTGGCCACCCAGTTGGGCTGCCCTTCCCACTCAGGCGAG	561
Oy	847	GAGCCGAAGAGAGGTTTGTGGGG	871
Db	562	GAGCCGAAGAGAGGTTTGTGGGG	586

RESULT	12
LOCUS	S67320
DEFINITION	alpha 2-adrenergic receptor [rat, Sprague-Dawley, 22 month old pancreas, mRNA Partial, 249 nt].
ACCESSION	S67320
VERSION	S67320.1 GI:456953
KEYWORDS	
SOURCE	Rattus sp.
ORGANISM	Rattus sp. Eutheria; Chordata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 249) Wang S.Y. and Pilkey D.T. Identification in islets of Langerhans of a new rat alpha 2-adrenergic receptor
AUTHORS	Diabetes 43 (1), 127-136 (1994)
TITLE	8262309
JOURNAL	GenBank staff at the National Library of Medicine created this entry [NCBI gibseq 140734] from the original journal article.
MEDLINE	This sequence comes from Fig. 1.
PUBMED	Location/Qualifiers
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FEATURES	1..249 partial /gene="alpha 2-adrenergic receptor"
source	41 a 99 c 64 g 45 t
BASE COUNT	
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Best Local Similarity	100.0%; Pred. NO. 3.7e-106;
Matches 230; Conservative	0; Mismatches 0; Indels 0; Gaps 0

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Db 221 GTGTACTGGCGCTCGA 237

RESULT 15

S67317S2

246 bp mRNA linear ROD 26-FEB-1994

alpha 2-adrenergic receptor (rats, Sprague-Dawley, 5 month old
pancreas, mRNA Partial, 246 nt, segment 2 of 2).S67319
S67319.1 GI:456951

VERSION

2 of 2

SEGMENT

SOURCE

ORGANISM

Rattus sp.

Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 246)

Wang, S.Y. and Pilkey, D.T.

Identification in islets of Langerhans of a new rat alpha

2-adrenergic receptor

Diabetes 43 (1), 127-136 (1994)

94085695

8262309

PUBMED

REMARK

Genbank staff at the National Library of Medicine created this

entry [NCBI glibbag 140733] from the original journal article.

This sequence comes from Fig. 1.

Location/Qualifiers

1..246

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/mol_type="mRNA"

/db_xref="taxon:10118"

order(S67317.1:1..130.1..246)

/gene="alpha 2-adrenergic receptor"

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BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 132; DB 10; Length 246;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 130 CTGGCCACCTTACGTGGCCAGTGTCTCTGGCCAGGAGGCGTGTATAGTGGGAG 189

QY 1066 TGGTGGCGTCTGA 1077

Db 190 TGGTGGCGTCTGA 201

Search completed: February 8, 2004, 04:51:26
Job time : 5127.53 secs



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Db 841 GCGCCAGGGCCAGAGAGAGAGTGTGGTGTGGGGGCACTCTCAGAGATGAAGCTGAAGAG 900
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RESULT 2
US-09-825-923-1
Sequence 1. US20010016338A1

GENERAL INFORMATION:

APPLICANT: Snapit, Amir
APPLICANT: Heimonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Koulou, Markku
APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuomala, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Nyysanen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Kaunonen, Jussi

APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIORITY APPLICATION NUMBER: 09/422,985
PRIORITY FILING DATE: 2000-05-25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein

US-09-825-923-1

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1341; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 121 CGCTGCTGCGGCGGCTCTCAGAACTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
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 ; Sequence 1, Application US/10077870
 ; Publication No. US20030003470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Salomon, Jukka T
 ; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
 ; FILE REFERENCE: 0933-0183P
 ; CURRENT APPLICATION NUMBER: US/10/077, 870
 ; PRIOR FILING DATE: 2002-05-21
 ; PRIOR APPLICATION NUMBER: FI 20010323
 ; PRIOR FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 1
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 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1341)
 ; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
 US-10-077-870-1

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QY	121	CGCTGCTGCGGCGCCCTCAGAACCTGTCTGTGTGCTGAGCGCGCCGACATCTCTG	180
Db	121	CGCTGCTGCGGCGCCCTCAGAACCTGTCTGTGTGCTGAGCGCGCCGACATCTCTG	180
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Db	421	GCGGTCACTCTGCTGCGGCGCCCTCATCTCAAGAGGCGACAGGAGCCCGCAGCGGAG	480
QY	481	CGCCCCAGTGCAGAGCTCAACCAAGAGGCGCTGTATCTCTGGCTTCAGCATCGATCT	540
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; FEATURE:
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; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2b-adrenoceptor protein
US-10-077-870-3

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Db	241	CGGCGCAC	GTGTGTGTGGAGGTGTATCTGTGGCGCTCGAGCTGTCTTTCGACCTTGTCATC	300
OY	301	GTGCAC	CTGTGTGCGCATCAGCTTGAACCGCTACTGGGCGGTGAGCCGCGCTGAGTAC	360
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OY	361	AAC	TCCAAAGCCGACCCCGGCGGCAGTATCATCTCTCATCTGTGTGTCATCTGCC	420
Db	361	AAC	TCCAAAGCCGACCCCGGCGGCAGTATCATCTCTCATCTGTGTGTCATCTGCC	420
OY	421	GCCGT	CATCTCGCTGCGCGCCCTCATCTTCAAGAGGCGAACAGGCGCCCGACCGCGGG	480
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OY	481	CGCCCC	AGTGCAGCTCAACAGAGGCGCTGTATCATCTTGCGCTTCAGACATCGATCT	540
Db	481	CGCCCC	AGTGCAGCTCAACAGAGGCGCTGTATCATCTTGCGCTTCAGACATCGATCT	540
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OY	601	CGCAG	CAACCGCAGAGGTCCACAGGCGCAAGGGGGGGCGTGGGCAAGGATGATCCAGACAG	660
Db	601	CGCAG	CAACCGCAGAGGTCCACAGGCGCAAGGGGGGGCGTGGGCAAGGATGATCCAGACAG	660
OY	661	CCCCG	ACCGACCATGTGTGGGGCTTTGGCTCAGCCAACTGCGACGCTGTGCTGTG	720
Db	661	CCCCG	ACCGACCGGACCATGTGTGGGGCTTTGGCTCAGCCAACTGCGACGCTGTGCTGTG	720
OY	721	GCTT	CTTGCACAGAGGTCAACGGAACCTGGAAGTCACTGGGGAGAAAGAGGGGGAG	780
Db	721	GCTT	CTTGTGCACAGAGGTCAACGGAACCTGGAAGTCACTGGGGAGAAAGAGGGGGAG	780
OY	781	ACCC	CTGAAGATCTGGGACCGGGGCTTGGCAACCCAGTTGGGCTGSCCTTCCCACTCA	840
Db	781	ACCC	CTGAAGATCTGGGACCGGGGCTTGGCAACCCAGTTGGGCTGSCCTTCCCACTCA	840
OY	841	GCGC	AGGCGCAGAGAGGCTTTGTGTGGGACATCTCCAGAGATGAAGCTGAAGAGAG	900
Db	841	GCGC	AGGCGCAGAGAGGCTTTGTGTGGGACATCTCCAGAGATGAAGCTGAAGAGAG	900
OY	901	GA	902	
Db	901	GA	902	

RESULT 6

US-10-001-073-1
; Sequence 1, Application US/10001073

; Publication No. US20030113725A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:

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; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten

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; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT

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; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01

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; NUMBER OF SEQ ID NOS: 53
;
; SOFTWARE: PatentIn Ver. 2.0.0

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; SEQ ID NO 1
; LENGTH: 1353

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; TYPE: DNA
; ORGANISM: Homo sapiens

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US-10-001-073-1

Query Match	67.1%	Score 902	DB 15	Length 1353
Best Local Similarity	100.0%	Pred. No. 0		
Matches 902	Conservative 0	Mismatches 0	Indels 0	Gaps 0

OY	1	ATGAGCAACCGAGGACCCCTATCCGTGAGGGCCACAGCGGCATAGAGGGCGGGCCATACG	60
Db	1	ATGAGCAACCGAGGACCCCTACTCCGTGAGGGCCACAGCGGCATAGAGGGCGGGCCATACG	60
OY	61	TTCTCATTTCTTTACCATCTTGCGCAACGCTCTGATCATCTGAGCTGTGGACAGC	120
Db	61	TTCTCATTTCTTTACCATCTTGCGCAACGCTCTGAGTCATCTGAGCTGTGGACAGC	120
OY	121	CGCTCGTCGCGCGCCCTCAGAACCTGTTCTTGATGTGCTGCGCGCGCGCGCAATCCTG	180
Db	121	CGCTCGTCGCGCGCCCTCAGAACCTGTTCTTGATGTGCTGCGCGCGCGCGCAATCCTG	180
OY	181	GTGGCAACGCTCATCATCCCTTTCTCGGTGCGCAACGAGGCTGTGGGCTATCTGGATCTT	240
Db	181	GTGGCAACGCTCATCATCCCTTTCTCGGTGCGCAACGAGCTGTGGGCTATCTGGATCTT	240
OY	241	CGGCGCAAGTGTGTCAGAGTGTACTGTGCGCTCGACGTCCTTTCTGCACTCGTGCATC	300
Db	241	CGGCGCAAGTGTGTCAGAGTGTACTGTGCGCTCGACGTCCTTTCTGCACTCGTGCATC	300
OY	301	GTGCACTGTGTGCGCATCAGCTTGGACCGCTACTGTGGCCGTGTAGCCCGGCGCTTGAATAC	360
Db	301	GTGCACTGTGTGCGCATCAGCTTGGACCGCTACTGTGGCCGTGTAGCCCGGCGCTTGAATAC	360
OY	361	AACTCGAAGGCGACCCCGCGCGCGGATCAAGGATCAATCCCTACATGTGTGGCTATCGCC	420
Db	361	AACTCGAAGGCGACCCCGCGCGCGGATCAAGGATCAATCTTCACTGTGTGGCTATCGCC	420
OY	421	GCGGTCAATCTTGCTGCGCGCCCTCATCTACAGGGGCGACCAAGGGCCCCCAGCCGCGGG	480
Db	421	GCGGTCAATCTTGCTGCGCGCCCTCATCTACAGGGGCGACCAAGGGCCCCCAGCCGCGGG	480
OY	481	CGCCCCCAGTGCAGAGCTCAGCAGAGAGGCGTGTATCATCTGTGGCTTCAGATGTGATCT	540
Db	481	CGCCCCCAGTGCAGAGCTCAGCAGAGAGGCGTGTATCATCTGTGGCTTCAGATGTGATCT	540
OY	541	TTCTTTGTGCTTGTGCTCATCATGATCCTTGTACACGCGGCGCATCTACCTGATCGCCAAA	600
Db	541	TTCTTTGTGCTTGTGCTCATCATGATCCTTGTGTACTGTGCGCATCTACCTGATCGCCAAA	600
OY	601	CGCAGCAACCGCAGAGGTCCCAAGGGCCCAAGGGGGGGGCTGTGGCAGGGTGAATCCAAAGAG	660
Db	601	CGCAGCAACCGCAGAGGTCCCAAGGGCCCAAGGGGGGGGCTGTGGCAGGGTGAATCCAAAGAG	660
OY	661	CCCGGACCCGACCATGTGTGGGGCTTTTGGCTCAGCCCAAATGTGCCAGCCCTGTGTG	720
Db	661	CCCGGACCCGACCATGTGTGGGGCTTTTGGCTCAGCCCAAATGTGCCAGCCCTGTGTG	720

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Qy 721 GCTTCTGACAGAGAGTCAAGCACTCCAACTCCTGGGGAAGAGAGAGGAGGAG 780
Db 721 GCTTCTGACAGAGAGTCAAGCACTCCAACTCCTGGGGAAGAGAGAGGAGGAG 780
Qy 781 ACCCTGAAGATCTAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 781 ACCCTGAAGATCTAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Qy 841 GGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 841 GGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Qy 901 GA 902
Db 901 GA 902

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RESULT 7

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US-10-305-720-1181
; Sequence 1181, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Expression
; FILE REFERENCE: PR-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1181
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181

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Query Match 67.1%; Score 902; DB 12; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGAGACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Db 413 ATGAGACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Qy 61 TTCTCATTTCTTTTACCATCTTGGGCAAGCCTCTGGTCACTTGGTGTGAGGAGGAG 120
Db 473 TTCTCATTTCTTTTACCATCTTGGGCAAGCCTCTGGTCACTTGGTGTGAGGAGGAG 120
Qy 121 CGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 533 CGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy 533 CGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 181 GTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Qy 593 GTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Db 241 CGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Qy 653 CGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db 713 GTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 301 GTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 713 GTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 361 AATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 773 AATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy 421 GCGTCAATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480

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Db 833 GCGTCAATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 892
Qy 481 CGCCCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 893 CGCCCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Qy 541 TTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 953 TTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Qy 601 CGAGCAACCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 1013 CGAGCAACCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy 661 CGCCGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 1073 CGCCGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Qy 721 GCTTCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 1133 GCTTCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Qy 781 ACCCTGAAGATCTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 1193 ACCCTGAAGATCTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Qy 841 GGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 1253 GGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Qy 901 GA 902
Db 1313 GA 1314

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RESULT 8

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US-10-225-567A-41
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41

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Query Match 67.1%; Score 902; DB 15; Length 3274;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGAGACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Db 1 ATGAGACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Qy 61 TTCTCATTTCTTTTACCATCTTGGGCAAGCCTCTGGTCACTTGGTGTGAGGAGGAG 120
Db 61 TTCTCATTTCTTTTACCATCTTGGGCAAGCCTCTGGTCACTTGGTGTGAGGAGGAG 120
Qy 121 CGCTCAATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180

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Db 121 CGCTGCTGGGCGCCCTCAGAACCTGTTCCTGGTGTGCTGGCCGCCGCGACATCTG 180
Qy 181 GTGGCCAGCGCTCATCATCCCTTTCTCGCTGGCCAAAGAGCTGCTGGGCTACTGTACTTC 240
Db 181 GTGGCCAGCGCTCATCATCCCTTTCTCGCTGGCCAAAGAGCTGCTGGGCTACTGTACTTC 240
Qy 241 CGGGCCAGCTGTGTCGAGGTGTACTCTGCGCTGACGTGCTCTTCTGCACTCTGTCATC 300
Db 241 CGGGCCAGCTGTGTCGAGGTGTACTCTGCGCTGACGTGCTCTTCTGCACTCTGTCATC 300
Qy 301 GTGCACTGTGTGCGCCATCAGCTGAGCCGCTACTGGGCGCTGAGCCGGCGCTGAGTAC 360
Db 301 GTGCACTGTGTGCGCCATCAGCTGAGCCGCTACTGGGCGCTGAGCCGGCGCTGAGTAC 360
Qy 361 AACTCCAAAGGCAACCCGGCGCGCATGATGATCACTCTCACTGTGTGCTCATGATGCC 420
Db 361 AACTCCAAAGGCAACCCGGCGCGCATGATGATCACTCTCACTGTGTGCTCATGATGCC 420
Qy 421 GCGGTATCTGCTGCGCCGCTTCATCTAACAAGGGGCAACAAGGCGCCGACGCCGCGGG 480
Db 421 GCGGTATCTGCTGCGCCGCTTCATCTAACAAGGGGCAACAAGGCGCCGACGCCGCGGG 480
Qy 481 CGGCCCCAGTGCAAGCTCAACCAAGAGGCGCTGTACTCTGCTTCAGCATGATCT 540
Db 481 CGGCCCCAGTGCAAGCTCAACCAAGAGGCGCTGTACTCTGCTTCAGCATGATCT 540
Qy 541 TTCTTGTCTCTGCTTCATCATGATCTCTTGTCTTACTGCGCATCTTACTGCGCAA 600
Db 541 TTCTTGTCTCTGCTTCATCATGATCTCTTGTCTTACTGCGCATCTTACTGCGCAA 600
Qy 601 CGGAGCAACCGCAGAGGTCCAGGGGCGCAAGGGGGGCGTGGGCGAGGTGATCCAGACAG 660
Db 601 CGGAGCAACCGCAGAGGTCCAGGGGCGCAAGGGGGGCGTGGGCGAGGTGATCCAGACAG 660
Qy 661 CCCGACCCGACCAATGTGTGGGCTTTGAGCTTCAAGCAACTGCCAGGCTGTGTG 720
Db 661 CCCGACCCGACCAATGTGTGGGCTTTGAGCTTCAAGCAACTGCCAGGCTGTGTG 720
Qy 721 GCTTGTGCGCAGAGGTCAACGCACTCGAATGCCCTGGGAGAGAGAGAGAGAGAGAG 780
Db 721 GCTTGTGCGCAGAGGTCAACGCACTCGAATGCCCTGGGAGAGAGAGAGAGAGAGAG 780
Qy 781 ACCCTGGAATATCTGGGAGCCCGGCTTGGCAACCCAGTTGGGCTGCTTCCCACTCA 840
Db 781 ACCCTGGAATATCTGGGAGCCCGGCTTGGCAACCCAGTTGGGCTGCTTCCCACTCA 840
Qy 841 GGCACAGGCGCAGAGAGAGGTGTGTGTGGGCACTCTCAGAGATGAAGCTGAAGAGAG 900
Db 841 GGCACAGGCGCAGAGAGAGGTGTGTGTGGGCACTCTCAGAGATGAAGCTGAAGAGAG 900
Qy 901 GA 902
Db 901 GA 902
Qy 901 GA 902
Db 901 GA 902

RESULT 9
US-09-908-975-4848
; Sequence 4848, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: MASSEMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
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; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 3237
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4848
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-908-975-4848

Query Match
Best Local Similarity 100.0%; Score 65; DB 13; Length 65;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 642 GCAGGTGATGTCACAGAGCCCGACCGACGACATGTGTGGGCTTGGCTCAGCCAACT 701
Db 1 GCAGGTGATGTCACAGAGCCCGACCGACCGACGACATGTGTGGGCTTGGCTCAGCCAACT 60
Qy 702 GCCAG 706
Db 61 GCCAG 65

RESULT 10
US-09-908-975-19227
; Sequence 19227, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: MASSEMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; NUMBER OF SEQ ID NOS: 3237
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19227
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-19227

Query Match
Best Local Similarity 100.0%; Score 60; DB 13; Length 60;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 698 AACTGCCAGCGCTGCTGTGTGCTTCTGCGAGAGGTCAACGCACTCGAAGTCCA 757
Db 1 AACTGCCAGCGCTGCTGTGTGCTTCTGCGAGAGGTCAACGCACTCGAAGTCCA 60

RESULT 11
US-10-001-073-24
; Sequence 24, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1350
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Title: US-09-692-077D-1

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13: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US04_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US03_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US02_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353	100.0	1353	15	US-10-001-073-1 Sequence 1, Appli
2	1302	96.2	1353	9	US-09-825-923-3 Sequence 3, Appli
3	1302	96.2	1353	15	US-10-077-870-3 Sequence 3, Appli
4	1251	92.5	2072	12	US-10-305-720-1181 Sequence 1181, Ap
5	1251	92.5	3474	15	US-10-225-567A-41 Sequence 41, Appli
6	918	67.8	1344	9	US-09-825-923-1 Sequence 1, Appli
7	918	67.8	1344	15	US-10-077-870-1 Sequence 1, Appli
8	902	66.7	1344	15	US-10-001-073-2 Sequence 2, Appli
9	60	4.8	65	13	US-09-908-975-4848 Sequence 4848, Ap
10	60	4.4	60	13	US-09-908-975-4827 Sequence 1927, A
11	45	3.3	1350	15	US-10-001-073-24 Sequence 24, Appli
12	45	3.3	1350	15	US-10-001-073-25 Sequence 25, Appli
13	45	3.3	3604	12	US-10-305-720-1180 Sequence 1180, Ap
14	45	3.3	3653	15	US-10-225-567A-39 Sequence 39, Appli
15	39	2.9	463	11	US-09-918-995-29557 Sequence 29557, A

16	39	2.9	1382	12	US-10-305-720-1256 Sequence 1256, Ap
17	39	2.9	1382	13	US-10-101-510-754 Sequence 754, App
18	39	2.9	1758	13	US-10-101-510-450 Sequence 450, App
19	36	2.7	215980	11	US-09-972-546-16 Sequence 16, Appli
20	34	2.5	1374	15	US-10-001-073-42 Sequence 42, Appli
21	34	2.5	1386	15	US-10-001-073-40 Sequence 40, Appli
22	34	2.5	2826	15	US-10-225-567A-43 Sequence 43, Appli
23	33	2.4	6904	13	US-10-311-455-48 Sequence 48, Appli
24	32	2.4	5387	14	US-10-001-873-22 Sequence 22, Appli
25	32	2.4	5326	10	US-09-818-264-3 Sequence 3, Appli
26	30	2.2	171	9	US-09-864-761-29686 Sequence 29686, A
27	30	2.2	193	9	US-09-864-761-23094 Sequence 23094, A
28	30	2.2	311	9	US-09-864-761-27934 Sequence 27934, A
29	30	2.2	477	11	US-09-918-995-27029 Sequence 27029, A
30	30	2.2	485	9	US-09-864-761-11354 Sequence 11354, A
31	30	2.2	492	9	US-09-864-761-6378 Sequence 6378, Ap
32	30	2.2	506	9	US-09-864-761-13125 Sequence 13125, A
33	30	2.2	1922	15	US-10-125-237-86 Sequence 86, Appli
34	30	2.2	1922	15	US-10-105-891-86 Sequence 86, Appli
35	30	2.2	3069	13	US-10-317-835-2 Sequence 2, Appli
36	30	2.2	3254	13	US-10-317-835-3 Sequence 3, Appli
37	30	2.2	4242	13	US-10-317-835-1 Sequence 1, Appli
38	30	2.2	4571	13	US-10-317-835-4 Sequence 4, Appli
39	30	2.2	96599	12	US-10-085-117-100 Sequence 100, App

ALIGNMENTS

RESULT 1	US-10-001-073-1	Application US/10001073
1	Sequence 1, Appli	US-10-001-073-1
2	Publication No.	US20030113725A1
3	GENERAL INFORMATION:	
4	APPLICANT:	Liggett, Stephen
5	APPLICANT:	Small, Kirsten
6	TITLE OF INVENTION:	Alpha-2-adrenergic receptor polymorphisms
7	FILE REFERENCE:	13073-PCT
8	CURRENT APPLICATION NUMBER:	US/10/001,073
9	CURRENT FILING DATE:	2001-11-01
10	NUMBER OF SEQ ID NOS:	53
11	SOFTWARE:	PatentIn Ver. 2.0
12	SEQ ID NO 1	
13	LENGTH:	1353
14	TYPE:	DNA
15	ORGANISM:	Homo sapiens
16	US-10-001-073-1	
17	Query Match	100.0%; Score 1353; DB 15; Length 1353;
18	Best Local Similarity	100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
19	Matches 1353; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
20	1	ATGACACACAGAGACCCCTACTCGTGACAGCAGCGCCATAGCGGCGCATCACC 60
21	1	ATGACACACAGAGACCCCTACTCGTGACAGCAGCGCCATAGCGGCGCATCACC 60
22	61	TTTCCTATTCTCTTACCATCTTGGCAACGCTGTGATATCTGGCTGTGACAC 120
23	61	TTTCCTATTCTCTTACCATCTTGGCAACGCTGTGATATCTGGCTGTGACAC 120
24	121	CGCTGCGGCGGCGCCCTAGAACGCTTCCGAGTGTGCGCGCGCGCGCATCCG 180
25	121	CGCTGCGGCGGCGCCCTAGAACGCTTCCGAGTGTGCGCGCGCGCGCATCCG 180
26	181	GTGGCAGCAGTATATCCCTTCTCGTGGCAACGAGCTGAGGCTACTGATCTTC 240
27	181	GTGGCAGCAGTATATCCCTTCTCGTGGCAACGAGCTGAGGCTACTGATCTTC 240
28	241	GTGGCAGCAGTATATCCCTTCTCGTGGCAACGAGCTGAGGCTACTGATCTTC 240
29	241	GTGGCAGCAGTATATCCCTTCTCGTGGCAACGAGCTGAGGCTACTGATCTTC 240
30	301	GTGGCAGCAGTATATCCCTTCTCGTGGCAACGAGCTGAGGCTACTGATCTTC 300
31	301	GTGGCAGCAGTATATCCCTTCTCGTGGCAACGAGCTGAGGCTACTGATCTTC 300

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Db | 301 | GTGACCTTGGCCCTACGACCTGAGACCTACTGGCCGTGAGCCGCGCCCTGAGATAC | 360 |
Qy | 361 | AACTCAAGGCGACCCCGCGCGCATCAAGTSCATCATCTCTCATCTGTGTGCTATGCCC | 420 |
Db | 361 | AACTCAAGGCGACCCCGCGCGCATCAAGTSCATCATCTCTCATCTGTGTGCTATGCCC | 420 |
Qy | 421 | GCGGTATCTCTGCTGCGCCCTCATCTCAAGGCGCGACAGGCGCCGCGCGCGCGCG | 480 |
Db | 421 | GCGGTATCTCTGCTGCGCCCTCATCTCAAGGCGCGACAGGCGCCGCGCGCGCGCGCG | 480 |
Qy | 481 | CGCCCGCATGCAAGCTCAACAGAGGCTGTATCATCTGCTGCTGCTGCTGCTGCTGCT | 540 |
Db | 481 | CGCCCGCATGCAAGCTCAACAGAGGCTGTATCATCTGCTGCTGCTGCTGCTGCTGCT | 540 |
Qy | 541 | TTCTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 600 |
Db | 541 | TTCTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 600 |
Qy | 601 | CGCAGCAACCGCAAGGCTCCAGGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCG | 660 |
Db | 601 | CGCAGCAACCGCAAGGCTCCAGGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | 660 |
Qy | 661 | CCGCGACCCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 720 |
Db | 661 | CCGCGACCCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 720 |
Qy | 721 | GCTTGTGCAAGAGGTCAAGGCACTGCAAGTCACTGCAAGTCACTGCAAGTCACTGCA | 780 |
Db | 721 | GCTTGTGCAAGAGGTCAAGGCACTGCAAGTCACTGCAAGTCACTGCAAGTCACTGCA | 780 |
Qy | 781 | ACCCTGAAATATCTGAGACCCGCGCTTGCACCCGCTGCTGCTGCTGCTGCTGCTGCT | 840 |
Db | 781 | ACCCTGAAATATCTGAGACCCGCGCTTGCACCCGCTGCTGCTGCTGCTGCTGCTGCT | 840 |
Qy | 841 | GCGCAGGCGCAGAGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 900 |
Db | 841 | GCGCAGGCGCAGAGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 900 |
Qy | 901 | GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 960 |
Db | 901 | GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 960 |
Qy | 961 | TCACTTGAAGCCCGCTGCAAGCAGCAGAGGCTCCCGGCTGCTGCTGCTGCTGCTGCT | 1020 |
Db | 961 | TCACTTGAAGCCCGCTGCAAGCAGCAGAGGCTCCCGGCTGCTGCTGCTGCTGCTGCT | 1020 |
Qy | 1021 | GCGCAGGTGCTCTGCGGCAAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1080 |
Db | 1021 | GCGCAGGTGCTCTGCGGCAAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1080 |
Qy | 1081 | GCGCAGGTGCTCTGCGGCAAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1140 |
Db | 1081 | GCGCAGGTGCTCTGCGGCAAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1140 |
Qy | 1141 | GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1200 |
Db | 1141 | GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1200 |
Qy | 1201 | TGCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1260 |
Db | 1201 | TGCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1260 |
Qy | 1261 | CTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1320 |
Db | 1261 | CTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1320 |
Qy | 1321 | CTGTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1380 |
Db | 1321 | CTGTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1380 |
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RESULT 2

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US-09-825-923-3
; Sequence 3, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapit, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulou, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Tuomola, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Myllynen, Riihtela
; APPLICANT: Salonen, Riihtela
; APPLICANT: Kaunonen, Veli-Pekka
; APPLICANT: Valtonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
; OTHER INFORMATION: protein
US-09-825-923-3
Query Match 96.2%; Score 1302; DB 9; Length 1353;
Best Local Similarity 99.9%; Freq. No. 0; Mismatches 1; Indels 0; Gaps 0;
Matches 1352; Conservative 0;
1 ATGAGCAACACAGACCCCTACTCCGTGCAAGCCAGCGCCATAGCGCGCCATACACC 60
1 ATGAGCAACACAGACCCCTACTCCGTGCAAGCCAGCGCCATAGCGCGCCATACACC 60
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61 TTCTCATTTCTTTTACCATCTTGGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
121 CGTTCGCTGCGGCGCCCTGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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421 GCGGTATCTCTGCTGCGCCCTCATCTCAAGGCGCGACAGGCGCCGCGCGCGCGCGCGCG 480
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QY 481 CCCCCCAGTGAAGCTCAACGAGAGGCTGTACATCTGCTCCAGATCGGATCT 540
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Db 481 CCCCCCAGTGAAGCTCAACGAGAGGCTGTACATCTGCTCCAGATCGGATCT 540
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QY 541 TTCTTGTCTCTTGTCTCATATGATCTTTGTCTACCTGCGATCTTACTTATCCGCAAA 600
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QY 661 CCCCCCAGCAGATGATGAGGGCTTTGAGCTCAGCCAACTGCAAGCCCTGAGCTCTGTG 720
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QY 721 GCTTCTGCAGAGAGGTCAACGAGCACTCGAAGTCCACTGGGAGAGAGAGAGAGAG 780
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Db 841 GGCAGAGGCGCAGAGAGAGGAGTGTGTTGTGGGGCATCTCGAAGATGAGAGAGAG 900
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Db 901 GAAAGAGAGAGAGAGAGAGAGAGAGTGTGAACCCAGAGCAGTGCAGTGTCTCCGAGC 960
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Db 1021 GGCAGAGTGTCTCTGAGGAGAGGGGGCGTGGTGTATGAGTGGGAGTGGGGTGGAGAG 1080
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QY 1081 GCGCAGAGTGAACCCGGGAGAGAGGCTTCACTTCTGTGCTGCTGTGTGCTATTTT 1140
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RESULT 3
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salomon, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
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; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3

Query Match          96.2%; Score 1302; DB 15; Length 1353;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 TTCTCATTTCTTTTAACTTTCGCGCAACGCTGTGTATCTGTGCTGTGTGTAACCAAC 120
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Db 61 TTCTCATTTCTTTTAACTTTCGCGCAACGCTGTGTATCTGTGCTGTGTGTAACCAAC 120
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QY 121 CGCTGCTGCGGCGCCCTCAGAACCTGTTCTGTGTGTGCTGAGCGCGCCGACATCTTG 180
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Db 181 GTGGCAGCGCTCATATCCCTTTCTGTGAGCAAGAGCTGTGAGGCTACTGTGATCTTC 240
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QY 241 CCGCGCAGTGTGTGAGAGGTATCTGTGAGCTGTGAGCTTCTTGTGACCTTGTCTATC 300
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QY 481 CCCCCCAGTGAAGCTCAACGAGAGGCTGTATCATCTGAGCCCTCCAGATCGGATCT 540
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Db 481 CCCCCCAGTGAAGCTCAACGAGAGGCTGTATCATCTGAGCCCTCCAGATCGGATCT 540
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Db 541 TTCTTGTCTCTTGTCTCATATGATCTTTGTCTACCTGCGATCTTACTTATCCGCAAA 600
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QY 601 CGCAGAACCGGAGAGGTCCAGGGCCAGAGGGGGGGCTGGGAGGGGTAGTCCAGCAG 660
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QY 661 CCCCCCAGCAGATGATGAGGGCTTTGAGCTCAGCCAACTGCAAGCCCTGAGCTCTGTG 720
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Db 661 CCCCCCAGCAGATGATGAGGGCTTTGAGCTCAGCCAACTGCAAGCCCTGAGCTCTGTG 720
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Db 721 GCTTCTGCAGAGAGGTCAACGAGCACTCGAAGTCCACTGGGAGAGAGAGAGAGAGAG 780
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QY 781 ACCCTTGAAAGATATCTGGGACCCGGGGCTTGGCCAACTGTTGGCTGCTTCCAACTCA 840
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Db 1613 TGCAGGTGCCCCCATGAGCTCTTCCAGTTCTTCTGATGCGCTACTGCAACAGCTCA 1672
Qy 1261 CTGAACCTGTATCTATACATCTTCAACAGAGACTTCGCGGTGCTTCCGAGATC 1320
Db 1673 CTGAACCTGTATCTATACATCTTCAACAGAGACTTCGCGGTGCTTCCGAGATC 1732
Qy 1321 CTGTGCGCGCCGTGAGCCGAGAGCGCTGTGA 1353
Db 1733 CTGTGCGCGCCGTGAGCCGAGAGCGCTGTGA 1765

RESULT 5
US-10-225-567A-41
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biociences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roubert, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41

Query Match 92.5%; Score 1251; DB 15; Length 3274;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 ATGAGACCAAGAGACCCCTACTCCCTGAGCGGACAGCGGCTTACGGCGGAGATCACC 60
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Db 61 TTCTCTATCTCTTATACATCTTGGGCAAGCTGTGATCACTGTGCTGTGTTGACACAG 120
Qy 121 CGCTGCTGCGCGCCCTGAGAACTGTTCCTGTGTGTGCTGCGCGGCGGCAATCTTG 180
Db 121 CGCTGCTGCGCGCCCTGAGAACTGTTCCTGTGTGTGCTGCGCGGCGGCAATCTTG 180
Qy 181 GTGGCAGCTATATCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 181 GTGGCAGCTATATCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
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Db 241 CGGCGCAGGTGTGAGAGGTGATCTGTGCGCTGAGCTGTCTTCTGTGACCTGTGCATC 300
Qy 301 GTGCACTGTGCGCATCAGCTGAGCGCTACTGTGGCCGTGAGCGCGGCTGTGAGTAC 360
Db 301 GTGCACTGTGCGCATCAGCTGAGCGCTACTGTGGCCGTGAGCGCGGCTGTGAGTAC 360
Qy 361 AACTCCAAAGGACCCCGCGGCGCATCAAGTGTATCTCTCACTGTGTGTGTGTGTGTGT 420
Db 361 AACTCCAAAGGACCCCGCGGCGCATCAAGTGTATCTCTCACTGTGTGTGTGTGTGTGT 420
Qy 421 GCGGTATCTGCTGTGCGCGCTCATCTCAAGGAGGACCAAGGAGGAGGAGGAGGAGGAG 480
Db 421 GCGGTATCTGCTGTGCGCGCTCATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy 481 CGGCGCAGGTGTCAACCAAGAGGCGTGTATCTGTGCTGTGACATCGATCTGT 540
Db 481 CGGCGCAGGTGTCAACCAAGAGGCGTGTATCTGTGCTGTGACATCGATCTGT 540

Qy 541 TTCTTGTCTCTTGTGCTCATATGATCTTGTCTACTGTGCGATCTACTGTATGCGCAA 600
Db 541 TTCTTGTCTCTTGTGCTCATATGATCTTGTCTACTGTGCGATCTACTGTATGCGCAA 600
Qy 601 CGGAGCAACCGAGAGGTCTCCAGGCGCAAGGGGGGGCTGTGGCAGGTGTGTCAAGCAG 660
Db 601 CGGAGCAACCGAGAGGTCTCCAGGCGCAAGGGGGGGCTGTGGCAGGTGTGTCAAGCAG 660
Qy 661 CCCCGACCGACATGTGTGGGGCTTGTGCTGAGCCAACTGCGAGCCCTGGCTGTGTG 720
Db 661 CCCCGACCGACATGTGTGGGGCTTGTGCTGAGCCAACTGCGAGCCCTGGCTGTGTG 720
Qy 721 GCTTGTGCGAGAGGTCAACCGGACCTGAGAGTCTCACTGTGGGAGAGAGAGAGAGAGG 780
Db 721 GCTTGTGCGAGAGGTCAACCGGACCTGAGAGTCTCACTGTGGGAGAGAGAGAGAGAGG 780
Qy 781 ACCCTGAAGATATCTGGAGCCCGGGCTTGTGCAACCCAGTTGGGCTGCTTCCAACTCA 840
Db 781 ACCCTGAAGATATCTGGAGCCCGGGCTTGTGCAACCCAGTTGGGCTGCTTCCAACTCA 840
Qy 841 GGCAGGGGCGAGAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAAGTGAAGAGAG 900
Db 841 GGCAGGGGCGAGAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAAGTGAAGAGAG 900
Qy 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGTGAACCCAGGAGTGCAGTGTCTCCGGCC 960
Db 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGTGAACCCAGGAGTGCAGTGTCTCCGGCC 960
Qy 961 TGAAGTTGAGCCCGCGCTGTGAGAGCAAGAGGCTCCCGGGTGTGGCCACCTTACGT 1020
Db 961 TGAAGTTGAGCCCGCGCTGTGAGAGCAAGAGGCTCCCGGGTGTGGCCACCTTACGT 1020
Qy 1021 GGCAGAGTCTCTGTGGGAGGGGCGGGGTGCTATATGTGGGAGTGTGGGTGGAAG 1080
Db 1021 GGCAGAGTCTCTGTGGGAGGGGCGGGGTGCTATATGTGGGAGTGTGGGTGGAAG 1080
Qy 1081 GCGCAGCTGACCCCGGAGAGAGGCTTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
Db 1081 GCGCAGCTGACCCCGGAGAGAGGCTTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
Qy 1141 GTGCTGT 1200
Db 1141 GTGCTGT 1200
Qy 1201 TGCAGAGTCCCGCATGTGCTCTTCCAGTCTTCTGTGTGTGTGTGTGTGTGTGTGT 1260
Db 1201 TGCAGAGTCCCGCATGTGCTCTTCCAGTCTTCTGTGTGTGTGTGTGTGTGTGTGT 1260
Qy 1261 CTGAACCTGTATCTATCAACATCTTCAACAGAGACTTCCGCGGTGCGAGAGATC 1320
Db 1261 CTGAACCTGTATCTATCAACATCTTCAACAGAGACTTCCGCGGTGCGAGAGATC 1320
Qy 1321 CTGTGCGCGCGGTGAGCCGAGAGCGGCTGTGA 1353
Db 1321 CTGTGCGCGCGGTGAGCCGAGAGCGGCTGTGA 1353

RESULT 6
US-09-825-923-1
; Sequence 1, Application US/09825923
; Patent No. US2001001638A1
; GENERAL INFORMATION:
; APPLICANT: Snapit, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulou, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A

[illegible]

RESULT 7
US-10-077-870-1
; Sequence 1, Amplified

: PUBLICATION US//10077870
 : PUBLICATION NO. US20030003470A1
 : GENERAL INFORMATION:
 : APPLICANT. 533

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; TITLE OF INVENTION:  Jukka T
; FILE REFERENCE:  Method for detecting
; CURRENT STATUS:

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CURRENT FILING DATE: 2002-05-21
 PRIOR APPLICATION NUMBER: US/10/077,870
 PRIOR APPLICATION NUMBER:

NUMBER FILING DATE: 2001-02-20
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentTri

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seq id no 1          ... ver. 3.1
length: 1344
type: dna
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 1
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LOC: CBS
LOCATION: (1) .. (1341)
OTHER INFORMATION: Co-27-
00-077

... coding sequence for variant human alpha-2B-adreno-

Local Similarity	Score 918;	DB 15;	Length 1344.
atches 918;	100.0%;	Pred. No. 0;	
Conservative			

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121 CGCTGCTGCAGCCCTCAGAACTGTTCCTGCATCGAC 120
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181 GGGGCCAGGCTCATTATCGTGTGTTCTGCCTGGCCGCCCCCATCTTG 180 -

181 GTGGCCACGCTATCATTCCTTTCTGGCTTCTCGTGCCACGAGCTGCTGGGGCTAACTGGTACTTC 242

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351 GTGACCTGTGGCCATCAGCCTGGACCGGCTGAGCCCGCGCTGAGATAC 350

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...TCTGCTGCTCATGCC 420


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Db      ||| 361 AACTCAGACGACCCCGCGCGCATCAAGTGCATCTCATCTGTGTGCTCATCGCC 420
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Db      ||| 422 GCGGTATCTCGCTGCGCGCCCTCATCTCAAGGGGACACAGGGCCCGCGCGCG 480
Qy      ||| 481 GCGCCCGACAGTCAACGAGAGGAGGCTGTACATCTGTGCTTCCAGATCGGATCT 540
Db      ||| 481 GCGCCCGACAGTCAACGAGAGGAGGCTGTACATCTGTGCTTCCAGATCGGATCT 540
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Qy      ||| 661 CCCCGACCCGACCATGTGTGGGCTTTTGGCTCTGACCCAACTGCGACGCTGTGCTGTG 720
Db      ||| 661 CCCCGACCCGACCATGTGTGGGCTTTTGGCTCTGACCCAACTGCGACGCTGTGCTGTG 720
Qy      ||| 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCCACTGTGGAGAGAGAGAGAGAGAG 780
Db      ||| 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCCACTGTGGAGAGAGAGAGAGAGAG 780
Qy      ||| 781 ACCCTGAGAGATCTGTGGACCCGCGGCTTGTCCACCCAGTTGGGCTGTGCTTCCCACTCA 840
Db      ||| 781 ACCCTGAGAGATCTGTGGACCCGCGGCTTGTCCACCCAGTTGGGCTGTGCTTCCCACTCA 840
Qy      ||| 841 GCGCAGGCGCAGAGAGGAGGTTTGTGTGGGACATCTCGAGAGATGAGCTGAGAGAGAG 900
Db      ||| 841 GCGCAGGCGCAGAGAGGAGGTTTGTGTGGGACATCTCGAGAGATGAGCTGAGAGAGAG 900
Qy      ||| 901 GAAGAGAGAGAGAGAGAG 918
Db      ||| 901 GAAGAGAGAGAGAGAGAG 918

```

```

RESULT 8
US-10-001-073-2
; Sequence 2, Application US//10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-2

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Query Match      66.7%; Score 902; DB 15; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGACACACGAGACCCCTACTCTCGTGACGCGCACAGCGGCATAGCGGCGGCATCACC 60
Db      1 ATGACACACGAGACCCCTACTCTCGTGACGCGCACAGCGGCATAGCGGCGGCATCACC 60
Qy      61 TTCTCATTTCTTTTACCATCTTTCGCAAGGCTGTGTATCTGTGCTGTGTGACCAAC 120
Db      61 TTCTCATTTCTTTTACCATCTTTCGCAAGGCTGTGTATCTGTGCTGTGTGACCAAC 120
Qy      121 GCGTGTGCGGCGCGCGCTCAGAACCTGTCTGTGTGCTGTGCGCGCGCGCATCTCG 180
Db      121 GCGTGTGCGGCGCGCGCTCAGAACCTGTCTGTGTGCTGTGCGCGCGCGCATCTCG 180

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Db      ||| 121 GCGTGTGCGGCGCGCGCTCAGAACCTGTCTGTGTGCTGTGCGCGCGCGCATCTCG 180
Qy      ||| 181 GTGGCAGAGCTCATATCCCTTCTGTGCGCAAGAGCTGTGGGCTACTGTACTTC 240
Db      ||| 181 GTGGCAGAGCTCATATCCCTTCTGTGCGCAAGAGCTGTGGGCTACTGTACTTC 240
Qy      ||| 241 GCGCAGACGTGTGCGAGGAGTGTACTGTGCGCTGACAGTGTCTTCTGACCTGTTCATC 300
Db      ||| 241 GCGCAGACGTGTGCGAGGAGTGTACTGTGCGCTGACAGTGTCTTCTGACCTGTTCATC 300
Qy      ||| 301 GTGACACTGTGTGCGCATACGCTTGAACCGCTTACTGTGCGCGCGCGCTGTGAGTAC 360
Db      ||| 301 GTGACACTGTGTGCGCATACGCTTGAACCGCTTACTGTGCGCGCGCGCTGTGAGTAC 360
Qy      ||| 361 AACTCAGACGACCCCGCGCGCATCAAGTGCATCTCATCTGTGTGCTCATCGCC 420
Db      ||| 361 AACTCAGACGACCCCGCGCGCATCAAGTGCATCTCATCTGTGTGCTCATCGCC 420
Qy      ||| 421 GCGGTATCTCGCTGCGCGCCCTCATCTCAAGGGGACACAGGGCCCGCGCGCG 480
Db      ||| 421 GCGGTATCTCGCTGCGCGCCCTCATCTCAAGGGGACACAGGGCCCGCGCGCG 480
Qy      ||| 481 GCGCCCGACGTCAAGCTCAACGAGAGGCTGTGATCTGTGCTTCCAGATCGGATCT 540
Db      ||| 481 GCGCCCGACGTCAAGCTCAACGAGAGGCTGTGATCTGTGCTTCCAGATCGGATCT 540
Qy      ||| 541 TTCTTGTCTCTTGTCTCATATGATCTTGTCTTACCTGTGCGATCTTACCTGATCGCAAA 600
Db      ||| 541 TTCTTGTCTCTTGTCTCATATGATCTTGTCTTACCTGTGCGATCTTACCTGATCGCAAA 600
Qy      ||| 601 GCGACAGACCGAGAGTGTCCAGGGCCAAAGGGGGGCTGTGCGAGGATGTCAGACAG 660
Db      ||| 601 GCGACAGACCGAGAGTGTCCAGGGCCAAAGGGGGGCTGTGCGAGGATGTCAGACAG 660
Qy      ||| 661 CCCCGACCCGACCATGTGTGGGCTTTTGGCTCTGACCCAACTGCGACGCTGTGCTGTG 720
Db      ||| 661 CCCCGACCCGACCATGTGTGGGCTTTTGGCTCTGACCCAACTGCGACGCTGTGCTGTG 720
Qy      ||| 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCCACTGTGGAGAGAGAGAGAGAGAG 780
Db      ||| 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCCACTGTGGAGAGAGAGAGAGAGAG 780
Qy      ||| 781 ACCCTGAGAGATCTGTGGACCCGCGGCTTGTCCACCCAGTTGGGCTGTGCTTCCCACTCA 840
Db      ||| 781 ACCCTGAGAGATCTGTGGACCCGCGGCTTGTCCACCCAGTTGGGCTGTGCTTCCCACTCA 840
Qy      ||| 841 GCGCAGGCGCAGAGAGGAGTGTGTGTGGGACATCTCGAGAGATGAGCTGAGAGAGAG 900
Db      ||| 841 GCGCAGGCGCAGAGAGGAGTGTGTGTGGGACATCTCGAGAGATGAGCTGAGAGAGAG 900
Qy      ||| 901 GA 902
Db      ||| 901 GA 902

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```

RESULT 9
US-09-908-975-4848
; Sequence 4848, Application US//09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607

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Mon Feb 9 08:28:38 2004

us-09-692-077d-1.cligo.rnpb

Page 8

PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4848
LENGTH: 65
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-908-975-4848

Query Match
Similarity 100.0%; Score 65; DB 13; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 GCAGGTCATGTCACAGAGCCCGACCCGACATGTCGGGCTTTGGCTTCAAGCAACT 701
DB 1 GCAGGTCATGTCACAGAGCCCGACCCGACATGTCGGGCTTTGGCTTCAAGCAACT 60
QY 702 GCCAG 706
DB 61 GCCAG 65

RESULT 10
US-09-908-975-19227
Sequence 19227, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: MASSEMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FINGER, Simcha
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19227
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-19227

Query Match
Similarity 100.0%; Score 60; DB 13; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.6e-19;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 698 AACTGCCAGCCCTGCTGTCCTTCTGACAGAGCTCAAGGACACTCCAGCAACT 757
DB 1 AACTGCCAGCCCTGCTGCTTCTTGCAGAGAGTCAAGGACACTCCAGCAACT 60

RESULT 11
US-10-001-073-24
Sequence 24, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 1350

TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-24

Query Match
Similarity 100.0%; Score 45; DB 15; Length 1350;
Best Local Similarity 100.0%; Pred. No. 7.8e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCGTCATGTCGACCTGTGGCCGACCTGACCGCTACTGG 336
DB 355 TCGTCATGTCGACCTGTGGCCGACCTGACCGCTACTGG 399

RESULT 12
US-10-001-073-25
Sequence 25, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 1350
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-25

Query Match
Similarity 100.0%; Score 45; DB 15; Length 1350;
Best Local Similarity 100.0%; Pred. No. 7.8e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCGTCATGTCGACCTGTGGCCGACCTGACCGCTACTGG 336
DB 355 TCGTCATGTCGACCTGTGGCCGACCTGACCGCTACTGG 399

RESULT 13
US-10-305-720-1180
Sequence 1180, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: An-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1180
LENGTH: 3604
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 g178195
US-10-305-720-1180

Query Match
Similarity 100.0%; Score 45; DB 12; Length 3604;
Best Local Similarity 100.0%; Pred. No. 6.9e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCGTCATGTCGACCTGTGGCCGACCTGACCGCTACTGG 336
DB 2432 TCGTCATGTCGACCTGTGGCCGACCTGACCGCTACTGG 2476

RESULT 14
 US-10-225-567A-39
 ; Sequence 39; Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lifespan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burner, Glenn C.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 39
 ; LENGTH: 3653
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-225-567A-39

Query Match 3.3%; Score 45; DB 15; Length 3653;
 Best Local Similarity 100.0%; Pred. No. 6.9e-12;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCCTTCATCGTCGACCTGTGCGCCATCAGCCTGACCGCTACTGG 336
 |||||
 DB 1234 TCCTTCATCGTCGACCTGTGCGCCATCAGCCTGACCGCTACTGG 1278

RESULT 15
 US-09-918-995-29557
 ; Sequence 29557; Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 29557
 ; LENGTH: 463
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(463)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-29557

Query Match 2.9%; Score 39; DB 11; Length 463;
 Best Local Similarity 100.0%; Pred. No. 7.9e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1141 GTGCTGTGCTGTGCTTCCCTCTCTCTCAGCTACAGCCTG 1179
 |||||
 DB 51 GTGCTGTGCTGTGCTTCCCTCTCTCTCAGCTACAGCCTG 89

Search completed: February 8, 2004, 06:56:26
 Job time : 521.217 secs

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XX 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGGETT) LIGGETT S B.
PA (SMALL) SMALL K M.
XX
PI Lliggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52117.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
ES Claim 4; Page 144; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:
(a) obtaining a sample, having a polynucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and
(b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (A) (999ggcgggagccg) or (B) (999gcgcctgag) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. ephedrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolfosine, idazoxan, tolazoline, phenoltamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR (Genbank Accession AF009500), the sequence includes a 9 nucleotide variant (AA199906) at nucleotides 901-909, absent in the alpha-2BAR variant (AA199906).

Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 other;

Query Match	100.0%; Score 1353; DB 23; Length 1353;
Best Local similarity	100.0%; Score 1353; DB 23; Length 1353;

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Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Qy	ATGAGCACCAGGAGCCCTTACTCCGTGACAGGCGCAAGCGGCGCATATGCGCGGCATACAC	60
Db	1 ATGAGCACCAGGAGCCCTTACTCCGTGACAGGCGCAAGCGGCGCATATGCGCGGCATACAC	60
Qy	61 TTCTCATTTCTTTTACCATCTTGGCAACGCTGTGATCATCTGGCTGTTCAGAC	120
Db	61 TTCTCATTTCTTTTACCATCTTGGCAACGCTGTGATCATCTGGCTGTTCAGAC	120
Qy	121 CGCTCGGTGGCGCCCTCAGAACCGTTCCTGTGTGTGCGTGGCGCGCGCGGACATCTG	180
Db	121 CGCTCGGTGGCGCCCTCAGAACCGTTCCTGTGTGTGCGTGGCGCGCGCGGACATCTG	180
Qy	121 CGCTCGGTGGCGCCCTCAGAACCGTTCCTGTGTGTGCGTGGCGCGCGCGGACATCTG	180
Db	121 CGCTCGGTGGCGCCCTCAGAACCGTTCCTGTGTGTGCGTGGCGCGCGCGGACATCTG	180
Qy	181 GTGGCAACGCTCATCATCCCTTTCTGCTGGCAACGAGCTGTGGCTACTGTGATCTTC	240
Db	181 GTGGCAACGCTCATCATCCCTTTCTGCTGGCAACGAGCTGTGGCTACTGTGATCTTC	240
Qy	241 CGCGCAGCAGTGGTGGAGGTTACCTGGCGGCTCGACAGTCTTCTGTGACCTGTCATC	300
Db	241 CGCGCAGCAGTGGTGGAGGTTACCTGGCGGCTCGACAGTCTTCTGTGACCTGTCATC	300
Qy	301 GTGACACTGTGGCGCATACGCTTGACCGCTTACTGGGCGGTGAGCGCGCGCTGAGTAC	360
Db	301 GTGACACTGTGGCGCATACGCTTGACCGCTTACTGGGCGGTGAGCGCGCGCTGAGTAC	360

Accession	Sequence	Length
Db	GTGACCTGTGTGGCCATCAGGCTGGAGCGGCTACTGAGCGCGGTAGCGCGCGCTGGAGTAC	360
QY	AACTTCANAGCGACCCCGCGCGCGCATCAAGTGCATCATCTCACTGTGTGGTGCATCGCC	420
Db	AACTCAAGCGCACCCCGCGCGCGCATCAAGTGCATCATCTCACTGTGTGGTGCATCGCGC	420
QY	GCGGTGATCTCGCTGCGCGCGCGCTCATCTAACAAGGCGGACCAAGGCGCGCCCGCGCGG	480
Db	GCGGTGATCTCGCTGCGCGCGCGCTCATCTAACAAGGCGGACCAAGGCGCGCGCGCGG	480
QY	CGCGCCCGAGTCAAGCTCAACGAGGAGCGCTGATCATCTGTGGCCCGCGAGATCGGATCT	540
Db	CGCGCCCGAGTCAAGCTCAACGAGGAGCGCTGATCATCTGTGGCCCGCGAGATCGGATCT	540
QY	TTCTTTGTCCTGTGGCTGATCATATATCTTGTGTACCGCGGATCTACCTGATTCGGCAAA	600
Db	TTCTTTGTCCTGTGGCTGATCATATATCTTGTGTACCGCGGATCTACCTGATTCGGCAAA	600

QY	601	CGCAGCAACCCGACAGAGTCTCCAGGGCCCAAGGGGGGGGCGCTGGGCAAGGTGAGTCCAAAGCAG	660
Db	601	CGCAGCAACCCGACAGAGTCTCCAGGGCCCAAGGGGGGGGCGCTGGGCAAGGTGAGTCCAAAGCAG	660
QY	661	CCCCGACCCGACCACTGCTGGGGCTTTGGCCTCAGCCAAACTGCACGCCCTTGCTGTG	720
Db	661	CCCCGACCCGACCACTGCTGGGGCTTTGGCCTCAGCCAAACTGCACGCCCTTGCTGTG	720
QY	721	GCTTCTGCGAAGAGAGTTCACGACACTTCGAAATTCATCTGGGGAGAAAGAGAGGGGGAG	780
Db	721	GCTTCTGCGAAGAGAGTTCACGACACTTCGAAATTCATCTGGGGAGAAAGAGAGGGGGAG	780
QY	781	ACCCCTGAAGATCACTGGGACCCGGGCGCTTGGCCACCAGTTGGGGCTGCCCTTCCCAACTCA	840
Db	781	ACCCCTGAAGATCACTGGGACCCGGGCGCTTGGCCACCAGTTGGGGCTGCCCTTCCCAACTCA	840
QY	841	GGCCAGGGCCCAAGAGAGAGGTGTTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG	900
Db	841	GGCCAGGGCCCAAGAGAGAGGTGTTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG	900
QY	901	GAAGAGAGAGAGAGAGAGAGAGATGTGAACCCCAAGGCAGTGCCTCTCCGGCC	960
Db	901	GAAGAGAGAGAGAGAGAGAGAGATGTGAACCCCAAGGCAGTGCCTCTCCGGCC	960
QY	961	TCAAGCTTGCAGCCCCCGCTGCAGCAGCAACAGGGCTCCCGAGTGTGAGCCACCTCAAGT	1021
Db	961	TCAAGCTTGCAGCCCCCGCTGCAGCAGCAACAGGGCTCCCGAGTGTGAGCCACCTCAAGT	1021

Qy	1081	GCGCAGCTGACCCGGGAGAAGACGCTTCACTTCGTGCAGCTGATGGATTTG	1146
Dp	1081	GCGCAGCTGACCCGGGAGAAGACGCTTCACTTCGTGCAGCTGATGGATTTG	1146
Qy	1081	GCGCAGCTGACCCGGGAGAAGACGCTTCACTTCGTGCAGCTGATGGATTTG	1146
Dp	1081	GCGCAGCTGACCCGGGAGAAGACGCTTCACTTCGTGCAGCTGATGGATTTG	1146
Qy	1141	GTCGCTGTCTGATTGCCCTTCTTCTTGACGTACAGCCTGGGAGCATCTGCCCCGAAGCAC	1200
Dp	1141	GTCGCTGTCTGATTGCCCTTCTTCTTGACGTACAGCCTGGGAGCATCTGCCCCGAAGCAC	1200
Qy	1201	TGCAAGGTGACCCATGAGCGCTTCCTCCACTTCCTCTTGAAATCGGCTACTGGAACAAGCTCA	1266
Dp	1201	TGCAAGGTGACCCATGAGCGCTTCCTCCACTTCCTCTTGAAATCGGCTACTGGAACAAGCTCA	1266
Qy	1261	CTGAACCTGTTTAATTACAACCAATCTTCAACACAGAGCTTCGCGCTTGACCTTCGGAGATC	1320
Dp	1261	CTGAACCTGTTTAATTACAACCAATCTTCAACACAGAGCTTCGCGCTTGACCTTCGGAGATC	1320
Qy	1321	CTGTGCGCGCCCGTGAAACCAGAGCGGCTGTGTGA	1353
Dp	1321	CTGTGCGCGCCCGTGAAACCAGAGCGGCTGTGTGA	1353

AAD04762
ID AAD04762 standard; DNA; 1353 BP.
AC AAD04762;
XX
XX 04-JUL-2001 (first entry)
XX
XX Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX
XX Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
XX glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
XX norepinephrine; epinephrine; therapy; vascular contraction;
XX coronary artery; coronary heart disease; CHD; chronic angina pectoris;
XX acute myocardial infarction; AMI; Prinzmetal's variant; de.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1353
XX FT /*tag= a
XX FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
XX FT protein"
XX
XX WO200129082-A1.
XX
XX PD 26-APR-2001.
XX
XX PF 20-OCT-2000; 2000WO-FI00913.
XX
XX PR 22-OCT-1999; 99US-0422985.
XX
XX (JUVA-) JUVAANTIA PHARMA LTD OY.
XX
XX PI Snapiir A, Heinonen P, Alhopuro P, Karvonen M, Koulou M, Pesonen U;
XX Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Myysoenen K;
XX PI Salonen R, Kahanen J, Valkonen V;
XX
XX MPI: 2001-300318/31.
XX P-PSDB: AAE00990.
XX
XX DR New DNA molecule encoding variant specific adrenoceptor protein with
XX PT deletion of specific amino acids located in the third intracellular
XX PT loop of the polypeptide, for treating vascular contraction of coronary
XX PT arteries -
XX
XX PS Disclosure; Page 27-29; 37pp; English.
XX
XX CC The present sequence is a gene encoding human alpha2B-adrenoceptor
XX CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
XX CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
XX CC acids (amino acids 294-311), located in the third intracellular loop of
XX CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
XX CC Alpha2-AR mediate many of the physiological effects of the
XX CC catecholamines, norepinephrine and epinephrine. An antagonist of
XX CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
XX CC vascular contraction of coronary arteries and a disease involving
XX CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
XX CC clinically expressed as Prinzmetal's variant form or acute myocardial
XX CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
XX
XX SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
XX
XX Query Match 96.2%; Score 1302; DB 22; Length 1353;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 ATGAGACACGAGACCCCTACTCCGTCAGGCGGACGCGGCTTACGCGGCGGACACAC 60
XX DB 1 ATGAGACACGAGACCCCTACTCCGTCAGGCGGACGCGGCTTACGCGGCGGACACAC 60
XX
XX QY 61 TTCCTCATCTCTTACCATCTTGGCAAGCTGTGATCCTGCTGTGTTGACGAC 120
XX DB 61 TTCCTCATCTCTTACCATCTTGGCAAGCTGTGATCCTGCTGTGTTGACGAC 120

DB 61 TTCCTCATCTCTTACCATCTTGGCAAGCTGTGATCCTGCTGTGTTGACGAC 120
QY 121 CGCTGCTGCGGCGCCCTGAGAACCTGTTCTGTGTGCTGCGCGCGCGGACATCTCT 180
DB 121 CGCTGCTGCGGCGCCCTGAGAACCTGTTCTGTGTGCTGCGCGCGCGGACATCTCT 180
QY 181 GTGGCAGACCTCATCATCTCTTCTGTCGCGGACGAGCTGTGGGCTACTGTGTTCTTC 240
DB 181 GTGGCAGACCTCATCATCTCTTCTGTCGCGGACGAGCTGTGGGCTACTGTGTTCTTC 240
QY 241 CGGCGCAGCTGTGGCGAGGTGTAACCTGCGGCTGAGCTGTCTTCTGCACTGTCTCATC 300
DB 241 CGGCGCAGCTGTGGCGAGGTGTAACCTGCGGCTGAGCTGTCTTCTGCACTGTCTCATC 300
QY 301 GTGCACTGTGGCGCATCATGAGCTGAGCGGCTACTGAGCGGCGGCGGCTGAGTAC 360
DB 301 GTGCACTGTGGCGCATCATGAGCTGAGCGGCTACTGAGCGGCGGCGGCTGAGTAC 360
QY 361 AACTCCAGCGGACCCCGCGCGCATCATGAGCTGATCTCTCATCTGTGTGCTCATCGCC 420
DB 361 AACTCCAGCGGACCCCGCGCGCATCATGAGCTGATCTCTCATCTGTGTGCTCATCGCC 420
QY 421 GCGGTATCTCGCTGCGCCCTCATCTCAAGGCGGACCGAGCGCGCGCGCGCGCG 480
DB 421 GCGGTATCTCGCTGCGCCCTCATCTCAAGGCGGACCGAGCGCGCGCGCGCGCGCG 480
QY 481 CGCGCCGAGTGAAGTCAACGAGGCGCTGTATCATCTGCGCTCCAGCATCGGATCT 540
DB 481 CGCGCCGAGTGAAGTCAACGAGGCGCTGTATCATCTGCGCTCCAGCATCGGATCT 540
QY 541 TTCTTGTCTCTTGTCTCATCATGATCTGTGTCTTACCTGCGCATCTTACCTGCGCAAA 600
DB 541 TTCTTGTCTCTTGTCTCATCATGATCTGTGTCTTACCTGCGCATCTTACCTGCGCAAA 600
QY 601 CGCAGCAACCGAGAGCTCCCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
DB 601 CGCAGCAACCGAGAGCTCCCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 661 CCCCGACCGGACCATGTGGGCTTGTGGCTCAAGCGCAACCTGCGCGCTGTG 720
DB 661 CCCCGACCGGACCATGTGGGCTTGTGGCTCAAGCGCAACCTGCGCGCTGTG 720
QY 721 GCTTTCGACAGAGGTCAACGAGCACTGAGTCCATCTGCGGAGAGAGAGAGAGAG 780
DB 721 GCTTTCGACAGAGGTCAACGAGCACTGAGTCCATCTGCGGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTGAAGATATCTGGAACCGGCGCTTGCACCCAGTTGGGCTCCCTTCCCACTCA 840
DB 781 ACCCTGAAGATATCTGGAACCGGCGCTTGCACCCAGTTGGGCTCCCTTCCCACTCA 840
QY 841 GGCAGGCGGAGAGAGGCTGTTTGTGGGCTCTTCCAGAGATGAAGCTGAAGAGAG 900
DB 841 GGCAGGCGGAGAGAGGCTGTTTGTGGGCTCTTCCAGAGATGAAGCTGAAGAGAG 900
QY 901 GAAAG 960
DB 901 GAAAG 960
QY 961 TCAGCTTGAAGCGCCCGCTGAGCAGCAGAGGCTCCCGGCTGTGCGACCTTACGT 1020
DB 961 TCAGCTTGAAGCGCCCGCTGAGCAGCAGAGGCTCCCGGCTGTGCGACCTTACGT 1020
QY 1021 GGCAGGCTCTCTTGGGCGAGGCGGCTGTGCTATAGGTGGGAGAGGTGGCTGCAAG 1080
DB 1021 GGCAGGCTCTCTTGGGCGAGGCGGCTGTGCTATAGGTGGGAGAGGTGGCTGCAAG 1080
QY 1081 GGCAGGCTACCGGAGAGAGGCTTACCTTGTGCTGAGCTGTGCTGCTGCTGCTT 1140
DB 1081 GGCAGGCTACCGGAGAGAGGCTTACCTTGTGCTGAGCTGTGCTGCTGCTGCTT 1140
QY 1141 GTGCTCTGTGCTTCCCTTCTTCACTACAGCTAGCTGAGGCGGCTGCGGAGGAC 1200
DB 1141 GTGCTCTGTGCTTCCCTTCTTCACTACAGCTAGCTGAGGCGGCTGCGGAGGAC 1200

QY 1201 TGCAGGTCCTCCATGCTCTTCCAGTTCTTCTGTGATCGGCTACTGCAACAGCTCA 1260
DB 1201 TGAAGGTGCTCCATGAGCCCTTCCAGTTCTTCTGTGATCGGCTACTGCAACAGCTCA 1260
QY 1261 CTGAACCCCTGTTATCTTACACCATCTTCAACCAAGACTTCGCGCTGCTTCCGAGGATC 1320
DB 1261 CTGAACCCCTGTTATCTTACACCATCTTCAACCAAGACTTCGCGCTGCTTCCGAGGATC 1320
QY 1321 CTGTGCGCCCGTGAACCCGAGAGCGCTGTGA 1353
DB 1321 CTGTGCGCCCGTGAACCCGAGAGCGCTGTGA 1353

RESULT 3

AAD4389 standard; DNA; 1353 BP.

AC AAD4389;

DT 13-DEC-2002 (first entry)

DE Human alpha-2B-adrenoceptor gene.

KW Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;

KM hypertension; hypotensive; gene; ds.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1353

XX /product= "Human alpha-2B-adrenoceptor protein"

PN MO200266617-A1.

PD 29-AUG-2002.

PF 13-FEB-2002; 2002MO-F100113.

PR 20-FEB-2001; 2001FI-0000323.

PA (JURI-) JURILAB LTD OY.

PI Salonen J;

DR WPI; 2002-667063/71.

DR P-PSDB; AAE26534.

PT Detecting a risk of hypertension and targeting treatment in a subject

PT by determining the pattern of alleles encoding a variant

PS alpha-2-adrenoceptor -

PS Disclosure; Page 27-29; 35pp; English.

CC The invention relates to a method for detecting a risk of hypertension

CC by determining the pattern of alleles encoding a variant alpha-2B-

CC adrenoceptor (AR) protein. The methods and compositions of the invention

CC are useful for detecting risks and targeting treatment for hypertension.

CC The kit is also useful for selecting for clinical drug trials testing

CC the antihypertensive effect of compounds. The present sequence is human

CC alpha-2B-adrenoceptor gene.

SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;

Query Match 96.2%; Score 1302; DB 24; Length 1353;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCACACGAGACCCCTTACTCCGTGACGCGACACGCGCATAGCGGCGCATCAC 60

DB 1 ATGAGCACACGAGACCCCTTACTCCGTGACGCGACACGCGCATAGCGGCGCATCAC 60

QY 61 TTCTCATTTCTCTTTACATCTTTCGCAACGCTGTGATCCTGGCTGTGACCAAC 120
DB 61 TTCTCATTTCTCTTTACATCTTTCGCAACGCTGTGATCCTGGCTGTGACCAAC 120

QY 121 CGCTGGCTGGCGCCCTTCAGAACTGTTCTGTGTGCTGTGGCGCGCCGACATCTTG 180
DB 121 CGCTGGCTGGCGCCCTTCAGAACTGTTCTGTGTGCTGTGGCGCGCCGACATCTTG 180

QY 181 GTGGCAGCGCTATCATCCCTTCTCGCTGGCCAAAGAGCTGTGGGCTACTGTACTTC 240
DB 181 GTGGCAGCGCTATCATCCCTTCTCGCTGGCCAAAGAGCTGTGGGCTACTGTACTTC 240

QY 241 CGGCGCAGTGTGTGAGAGTGTACTGTGGGCTGACAGTGTCTTCTGCACTGTGTCATC 300
DB 241 CGGCGCAGTGTGTGAGAGTGTACTGTGGGCTGACAGTGTCTTCTGCACTGTGTCATC 300

QY 301 GTGCACTGTGTGCGCATGAGCTGTGACCGCTACTGTGGGCTGTAGCGCGCTGTGAGTAC 360
DB 301 GTGCACTGTGTGCGCATGAGCTGTGACCGCTACTGTGGGCTGTAGCGCGCTGTGAGTAC 360

QY 361 AACTCCAGCGCAGCCCGCGCGCATCAAGTGCATCATCTGATGTGCTCATTCGCC 420
DB 361 AACTCCAGCGCAGCCCGCGCGCATCAAGTGCATCATCTGATGTGCTCATTCGCC 420

QY 421 GCGGTATCTGCTGCGCGCCCTCATCTTCAAGAGCGACAGAGCGCCCGCGCGCG 480
DB 421 GCGGTATCTGCTGCGCGCCCTCATCTTCAAGAGCGACAGAGCGCCCGCGCGCG 480

QY 481 CGCCCCAGTGAAGCTCAACAGAGGCTGTGTATCTGTGGCTTCCAGCATTCGATTT 540
DB 481 CGCCCCAGTGAAGCTCAACAGAGGCTGTGTATCTGTGGCTTCCAGCATTCGATTT 540

QY 541 TTCTTGTGCTGCTGTGCTCATATGATCTGTGTCTACTGTGGCATCTACTGTGCAAA 600
DB 541 TTCTTGTGCTGCTGTGCTCATATGATCTGTGTCTACTGTGGCATCTACTGTGCAAA 600

QY 601 CGCAGCAACCGCAGAGTCCAGAGGCAAGAGGAGGAGCTGTGGCAGAGTGTCAAGCAG 660
DB 601 CGCAGCAACCGCAGAGTCCAGAGGCAAGAGGAGGAGCTGTGGCAGAGTGTCAAGCAG 660

QY 661 CCGGACCCGACATGATGTGGGCTTTGGCTTCAGCAAACTGCAAGCCCTGTGCTGTG 720
DB 661 CCGGACCCGACATGATGTGGGCTTTGGCTTCAGCAAACTGCAAGCCCTGTGCTGTG 720

QY 721 GCTTGTGCAAGAGATGACAGGACCTGGAAGTCACTGGAAGTCACTGTGGGAGAGAGGAG 780
DB 721 GCTTGTGCAAGAGATGACAGGACCTGGAAGTCACTGGAAGTCACTGTGGGAGAGAGGAG 780

QY 781 ACCCTTGAAGATCTGGAGCCCGGCTTGTGCACCCAGTTGGGCTGCCCTTCCAACTCA 840
DB 781 ACCCTTGAAGATCTGGAGCCCGGCTTGTGCACCCAGTTGGGCTGCCCTTCCAACTCA 840

QY 841 GGCAGGGCCAGAGAGAGGAGGTTGTGTGGGATCTTCCAGAGATGAAGCTGAAGAGAG 900
DB 841 GGCAGGGCCAGAGAGAGGAGGTTGTGTGGGATCTTCCAGAGATGAAGCTGAAGAGAG 900

QY 901 GAAG 960
DB 901 GAAG 960

QY 961 TCAGTTTCAAGCCCGCTGTGAGAGCAAGAGGCTCCCGGAGTGTGGCCACCTTAGT 1020
DB 961 TCAGTTTCAAGCCCGCTGTGAGAGCAAGAGGCTCCCGGAGTGTGGCCACCTTAGT 1020

QY 1021 GGCAGAGTGTCTGTGGAG 1080
DB 1021 GGCAGAGTGTCTGTGGAG 1080

QY 1081 GCGAGCTGAGCCCGGAG 1140
DB 1081 GCGAGCTGAGCCCGGAG 1140

QY 1141 GTGCTGTGCTGCTTCCCTTCTTCACTTCAAGCTGTGGGCGCATCTGCCAGAGCAGC 1200

Db	1141	GTGCTCTGCTGGTTCCTCCCTCTTCTTCTTACGCTACAGCCTTGCGGCGCCATCTGCCCGAAGAC	1200
Qy	1201	TGCAAGTGCCTCATGGCCTCTTCAGTTCCTTCTTGATCGGCTACTGCAACAGCTCA	1260
Db	1201	TGCAAGTGCCTCATGGCCTCTTTCAGTTCCTTCTTGATCGGCTACTGCAACAGCTCA	1260
Qy	1261	CTGAACCGCTGTTATATACACCATCTTCAACGAGACTTCGCGCGTTCCTCGGAGATC	1320
Db	1261	CTGAACCGCTGTTATATACACCATCTTCAACGAGACTTCGCGCGTTCCTCGGAGATC	1320
Qy	1321	CTGTGCGCGCCGTGGACCCAGACGGGCTGTGA	1353
Db	1321	CTGTGCGCGCCGTGGACCCAGACGGGCTGTGA	1353
RESULT 4			
ID	ACAS6583		
ID	ACAS6583	standard; CDNA; 2072 BP.	
AC	ACAS6583;		
XX			
DT	06-JUN-2003	(first entry)	
XX			
DE	Human signalling pathway polynucleotide probe SEQ ID NO 1181.		
XX			
KW	Human; probe; ss; array element; Parkinson's disease;		
KW	signalling pathway population; cancer; adenocarcinoma; leukaemia;		
KW	immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.		
XX			
OS	Homo sapiens.		
XX			
PN	US6500938-B1.		
XX			
PD	31-DEC-2002.		
XX			
PE	30-JAN-1998; 98US-0016434.		
XX			
PR	30-JAN-1998; 98US-0016434.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Au-Young J, Seilhamer JJ;		
XX			
DR	WP1; 2003-352189/33.		
XX			
PT	Combination of polynucleotide probes, useful as array elements in a		
PT	microarray for monitoring the expression of a number of target		
PT	polynucleotides -		
XX			
PS	Claim 1; SEQ ID NO 1181; 65bp; English.		
XX			
CC	The invention relates to a combination which, comprises a number of		
CC	polynucleotide probes comprising a sequence selected from one of the 1490		
CC	sequences mentioned in the specification. The combination is useful as an		
CC	array element in a microarray for monitoring the expression of a number		
CC	of target polynucleotides. The microarray is particularly useful in the		
CC	diagnosis and treatment of cancer and immunopathology and neuropathology.		
CC	The microarray is useful in diagnostics and treatment regimens, drug		
CC	discovery and development, toxicological and carcinogenicity studies,		
CC	forensics and pharmacogenomics. The microarray is also useful for		
CC	monitoring progression of diseases and for developing sophisticated		
CC	probes for the effects of currently available therapeutic drugs. The		
CC	combination is also useful for purifying a subpopulation of mRNAs, cDNAs		
CC	and genomic fragments and in research and diagnostic applications. The		
CC	array can detect changes in expression in a large number of genes coding		
CC	for different signalling pathway populations which can be used to diagnose		
CC	various diseases including cancer e.g. adenocarcinoma and leukaemia,		
CC	immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease		
CC	and Parkinson's disease. The present sequence represents a polynucleotide		
CC	probe of the invention.		
CC	Note: The sequence data for this patent did not form part of the printed		
CC	specification but was obtained in electronic format directly from USPO		

CC	at	seqdata.uspto.gov/sequence.html?docID=0650093881.
XX	Sequence	2072 BP; 316 A; 705 C; 660 G; 391 T; 0 other;
SQL	Query Match	92.5%; Score 1251; DB 25; Length 2072;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 1351; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1	ATGAGCACACGAGACCCCTACTCCGTGACAGGCGCACAGCGGCATAGCGCGGCATCAC
DB	413	ATGAGCACACGAGACCCCTACTCCGTGACAGGCGCACAGCGGCATAGCGGCATCAC
QY	61	TTTCCTCATCTCTTTAACATCTTTGGGCAAGCTCTGTATCTCCGTGTGTGACAGC
DB	473	TTTCCTCATCTCTTTAACATCTTTGGGCAAGCTCTGTATCTCCGTGTGTGACAGC
QY	121	CGCTCGCTGCGCGCCCTCAGAACCTGTCTCTGTGTGCTGTGCGCGCGCGCATCTG
DB	533	CGCTCGCTGCGCGCCCTCAGAACCTGTCTCTGTGTGCTGTGCGCGCGCGCATCTG
QY	181	GTGGCCACGCTCATATCCCTTTCTCGCTGCGCCACGAGCTGCTGGCTACTGTGACTTC
DB	593	GTGGCCACGCTCATATCCCTTTCTCGCTGCGCCACGAGCTGCTGGCTACTGTGACTTC
QY	241	CGCGGCACGTGTGTGCGAGGTATACCTGGCGCTCGAGTGTCTTCTGTGACTGTGCATC
DB	653	CGCGGCACGTGTGTGCGAGGTATACCTGGCGCTCGAGTGTCTTCTGTGACTGTGCATC
QY	301	GTGACACCTGTGCGGCATACGCTGTGAGACCGGCTACCTGTGAGCGCGCGCTGTGATAC
DB	713	GTGACACCTGTGCGGCATACGCTGTGAGACCGGCTACCTGTGAGCGCGCGCTGTGATAC
QY	361	AACCTCAAGCGCACCCCGCGCGCATGATGATCATCTCTACTGTGTGGCTCATCGCC
DB	773	AACCTCAAGCGCACCCCGCGCGCATGATGATCATCTCTACTGTGTGGCTCATCGCC
QY	421	GCGCTCATCTGTGCTGCGCGCCCTCATCTACAGGGCGACCAAGGGCCCCCAGCGCGGG
DB	833	GCGCTCATCTGTGCTGCGCGCCCTCATCTACAGGGCGACCAAGGGCCCCCAGCGCGGG
QY	481	CGCCCCAGTGTGCAAGCTCAACAGAGAGCGCTGTGATACCTGGCTCAGCATGTGATCT
DB	893	CGCCCCAGTGTGCAAGCTCAACAGAGAGCGCTGTGATACCTGGCTCAGCATGTGATCT
QY	541	TTCTTTGCTCCTTGTCTCATCATGATCCTTGTCTACCTGTGCGCATCTACTGATGCCAAA
DB	953	TTCTTTGCTCCTTGTCTCATCATGATCCTTGTCTACCTGTGCGCATCTACTGATGCCAAA
QY	601	CGAGCAACCGCAGAGGTCCAGGGGCCAAGGGGGGGCTGTGGCGAGGGTGTGATCCAGCAG
DB	1013	CGAGCAACCGCAGAGGTCCAGGGGCCAAGGGGGGGCTGTGGCGAGGGTGTGATCCAGCAG
QY	661	CCCCGACCCCAACATGTGTGGGGCTTTTGGGCTCAGCCCAAATGCGCAGGCCCTGTGTG
DB	1073	CCCCGACCCCAACATGTGTGGGGCTTTTGGGCTCAGCCCAAATGCGCAGGCCCTGTGTG
QY	721	GCTTCTGCGAGAGGTCTCAACGAGCATCTGAGTCTCACTGGGAGAGAGAGAGAGAGAG
DB	1133	GCTTCTGCGAGAGGTCTCAACGAGCATCTGAGTCTCACTGGGAGAGAGAGAGAGAGAG
QY	781	ACCCCTGAGATCTGAGGACCCCGGGCTTGTGCAACCAAGTTTGGGTGCTTCCCACTCA
DB	1193	ACCCCTGAGATCTGAGGACCCCGGGCTTGTGCAACCAAGTTTGGGTGCTTCCCACTCA
QY	841	GGCCAGGGCCCAAGAGAGGGTGTGTGTGGGGCATCTTCAAGAGATGAAGCTGAAGAGAG
DB	1253	GGCCAGGGCCCAAGAGAGGGTGTGTGTGGGGCATCTTCAAGAGATGAAGCTGAAGAGAG
QY	901	GAAAG
DB	1313	GAAAG
QY	961	TGACCTTGTGACGCCCGCGCTGTGACAGCACAGAGGCTCCGGGTGTGGCCACCTTACGT

QY 601 CCGAGCAACCGAGAGGTCCCAAGGCGCAAGGGGGGGCTTGAGGAGGTGATCCAAAGCAG 660
DB 601 CCGAGCAACCGAGAGGTCCCAAGGCGCAAGGGGGGGCTTGAGGAGGTGATCCAAAGCAG 660
QY 661 CCCCCCAACCGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 720
DB 661 CCCCCCAACCGAGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 720
QY 721 GCTTTCGAGAGAGGTGAGAGGAGCACTGGAAGTCCAGTGGGAGAGAGAGAGAGAGAGAG 780
DB 721 GCTTTCGAGAGAGGTGAGAGGAGCACTGGAAGTCCAGTGGGAGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTTGAGAGATCTGAGAGCCCGGGCTTGAGAGCCAGAGTGGAGTCCCTTCCCACTCA 840
DB 781 ACCCTTGAGAGATCTGAGAGCCCGGGCTTGAGAGCCAGAGTGGAGTCCCTTCCCACTCA 840
QY 841 GGGCAGAGGCGCAGAGAGAGGTGTTTGTGGGGCATCTTCAGAGAGATGAGTGAAGAGAG 900
DB 841 GGGCAGAGGCGCAGAGAGAGGTGTTTGTGGGGCATCTTCAGAGAGATGAGTGAAGAGAG 900
QY 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGTGAAGCCCGAGGAGTGCAGAGTCTCCGGCC 960
DB 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGTGAAGCCCGAGGAGTGCAGAGTCTCCGGCC 960
QY 961 TCAGCTTGAGAGCCCGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 TCAGCTTGAGAGCCCGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 GGGCAGAGTCTCTCTGAG 1080
DB 1021 GGGCAGAGTCTCTCTGAG 1080
QY 1081 GGGCAGAGTCTCTCTGAG 1140
DB 1081 GGGCAGAGTCTCTCTGAG 1140
QY 1141 GTGCTTGAGAGTCT 1200
DB 1141 GTGCTTGAGAGTCT 1200
QY 1201 TGCAGAGTCT 1260
DB 1201 TGCAGAGTCT 1260
QY 1261 CTGAGAGTCT 1320
DB 1261 CTGAGAGTCT 1320
QY 1321 CTGAGAGTCT 1380
DB 1321 CTGAGAGTCT 1380
RESULT 6
AAD04761
ID AAD04761 standard; DNA; 1344 BP.
XX
AC AAD04761;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
XX
KW Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW noradrenergic; epinephrine; therapy; vascular contraction; variant;
KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1344

FT /*tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT variant protein"
PN WO200129082-A1.
XX
XX 26-APR-2001.
PD
PF 20-OCT-2000; 2000WO-FI00913.
XX
XX 22-OCT-1999; 99US-0422985.
PR
XX (JUVVA-) JUVVANTIA PHARMA LTD OY.
XX
XX Snapper A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U,
PI Scheinin M, Salonen JT, Tuominen T, Lakka TB, Myrsoenen K,
PI Salonen R, Kauhainen J, Valkonen V;
XX
XX MPI; 2001-300318/31.
DR P-PSDB; AAE00389.
XX
XX New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular
PT loop of the polypeptide, for treating vascular contraction of coronary
PT arteries -
XX
XX Claim 3; Page 24-26; 37pp; English.
XX
XX The present sequence is a gene encoding human alpha2B-adrenoceptor
CC (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
CC element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
CC 18 amino acids (amino acids 294-311), located in the third intracellular
CC loop of the receptor polypeptide. The variant is obtained by deletion of
CC three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
CC gene is located on chromosome 2. Alpha2-AR mediate many of the
CC physiological effects of the catecholamines, norepinephrine and
CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
CC a mammal suffering from vascular contraction of coronary arteries and a
CC disease involving vascular contraction of coronary arteries which is
CC clinically expressed as coronary heart disease (CHD), unstable chronic
CC angina pectoris which is clinically expressed as Prinzmetal's variant
CC form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
CC gene therapy.
XX
XX Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
SQ
Query Match 67.8%; Score 918; DB 22; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGACACAG 60
DB 1 ATGAGACACAG 60
QY 61 TTCTCATCTCTCTTACATCTTGGCAAGAGTCTGATCTGAGTCTGTTGACAGC 120
DB 61 TTCTCATCTCTTTCATCTTGGCAAGAGTCTGATCTGAGTCTGTTGACAGC 120
QY 121 CGCTGCTGCGGCGCCCTCAGAACTGTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 180
DB 121 CGCTGCTGCGGCGCCCTCAGAACTGTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 180
QY 181 GTGGCAGAGTCTATCT 240
DB 181 GTGGCAGAGTCTATCT 240
QY 241 CGGCGCAGTGGAGAGAGTGAAGTCTGAGTCTGAGTCTCTTCTGACAGTCTGATCTGATC 300
DB 241 CGGCGCAGTGGAGAGAGTGAAGTCTGAGTCTGAGTCTCTTCTGACAGTCTGATCTGATC 300
QY 301 GTGACAGTCTGAG 360
DB 301 GTGACAGTCTGAG 360

OY	361	AAC	TCAAGGACACCCCGCCGATCAAAATGATATATCTCACTGTGTGCTATCGCC	422
Db	361	AAC	TCAAGGACACCCCGCCGATCAAAATGATATATCTCACTGTGTGCTATCGCC	422
OY	421	GCC	GATCTGTGTCGCGCCCTCATCTTCAAGAGGCGACCAAGGCCCCAGCGCGG	480
Db	421	GCC	GATCTGTGTCGCGCCCTCATCTTCAAGAGGCGACCAAGGCCCCAGCGCGG	480
OY	481	CGC	CCCAAGTGCATCAACCAAGAGGCTGTATCATCTTGACCTCCAGATCGATCT	540
Db	481	CGC	CCCAAGTGCATCAACCAAGAGGCTGTATCATCTTGACCTCCAGATCGATCT	540
OY	541	TTCT	TGTCCTTGCCATCATGATCTTGTCTACTGCGATTAATCTGATGCGCAA	600
Db	541	TTCT	TGTCCTTGCCATCATGATCTTGTCTACTGCGATTAATCTGATGCGCAA	600
OY	601	CGC	AGCAACGACAGAGTCCCAAGGACCAAGGGGGGCTGGGACAGGATCCACACG	666
Db	601	CGC	AGCAACGACAGAGTCCCAAGGACCAAGGGGGGCTGGGACAGGATCCACACG	666
OY	661	CCC	GACCCGACCATGATGAGGCTTTGGCTTCAGCCAACTGCCAGCCTGTGTG	720
Db	661	CCC	GACCCGACCATGATGAGGCTTTGGCTTCAGCCAACTGCCAGCCTGTGTG	720
OY	721	GCT	CTCCAGAGGTCAACGACCTGGAAGTCACTGGGAGAGAGAGAGGGGAG	780
Db	721	GCT	CTCTCCAGAGGTCAACGACCTGGAAGTCACTGGGAGAGAGAGAGGGGAG	780
OY	781	ACC	CTGAAATCTAGGACCCGGGCTTGGACACCAAGTGGGGCTGGCCCTCCCACTCA	840
Db	781	ACC	CTGAAATCTAGGACCCGGGCTTGGACACCAAGTGGGGCTGGCCCTCCCACTCA	840
OY	841	GGC	AGGCGCAAGAGAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG	900
Db	841	GGC	AGGCGCGCAAGAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG	900
OY	901	GAA	GAGAGAGAGAGAG 918	
Db	901	GAA	GAGAGAGAGAGAGAG 918	

RESULT	7
AAD44388	
ID	AAD44388 standard; DNA; 1344 BP.
XX	
AC	AAD44388;
XX	
DT	13-DEC-2002 (first entry)
XX	
DE	Human alpha-2B-adrenoceptor variant DNA.
XX	
KM	Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive,
XX	hypertension; hypotensive; variant; gene; ds.
OS	Homo sapiens.
XX	
XX	Synthetic.
Key	Location/Qualifiers
CDS	1..1344
FT	/*tag= a
FT	/product= "Human alpha-2B-adrenoceptor variant
FT	protein"
XX	
PN	MO200266617-A1.
XX	
PD	29-AUG-2002.
XX	
PF	13-FEB-2002; 2002WO-FI00113.
XX	
PR	20-FEB-2001; 2001FI-0000323.
XX	
PA	(JURI-) JURILAB LTD OY.

Query Match	Best Local Similarity	Score 918;	DB 24;	Length 1344;
Matches 918;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1 ATGGACACACAGAGCCCTTACTCGCTGAGAGCCACAGAGGCGCGCCGACATACC 60	1 ATGGACACACAGAGCCCTTACTCGCTGAGAGCCACAGAGGCGCGCCGACATACC 60			
1 ATGGACACACAGAGCCCTTACTCGCTGAGAGCCACAGAGGCGCGCCGACATACC 60	1 ATGGACACACAGAGCCCTTACTCGCTGAGAGCCACAGAGGCGCGCCGACATACC 60			
61 TTCTCATATCTCTTTACCATCTTGCGGCAAGCGCTGTGCATCTGGCTGTGTGACAGC 120	61 TTCTCATATCTCTTTACCATCTTGCGGCAAGCGCTGTGCATCTGGCTGTGTGACAGC 120			
61 TTCTCATATCTCTTTACCATCTTGCGGCAAGCGCTGTGCATCTGGCTGTGTGACAGC 120	61 TTCTCATATCTCTTTACCATCTTGCGGCAAGCGCTGTGCATCTGGCTGTGTGACAGC 120			
121 CGCTGCTGCGCGCCCTCAGAACCTGTTCTCGGGGTGCTGGCGCGCCCGGACATCCTG 180	121 CGCTGCTGCGCGCCCTCAGAACCTGTTCTCGGGGTGCTGGCGCGCCCGGACATCCTG 180			
121 CGCTGCTGCGCGCCCTCAGAACCTGTTCTCGGGGTGCTGGCGCGCCCGGACATCCTG 180	121 CGCTGCTGCGCGCCCTCAGAACCTGTTCTCGGGGTGCTGGCGCGCCCGGACATCCTG 180			
181 GTGCGCACGCTCATATCATCTTTCTGCTGGGCAACAGAGCTGTGGCTATCTGTACTTC 240	181 GTGCGCACGCTCATATCATCTTTCTGCTGGGCAACAGAGCTGTGGCTATCTGTACTTC 240			
181 GTGCGCACGCTCATATCATCTTTCTGCTGGGCAACAGAGCTGTGGCTATCTGTACTTC 240	181 GTGCGCACGCTCATATCATCTTTCTGCTGGGCAACAGAGCTGTGGCTATCTGTACTTC 240			
241 CGGCGCACGCTGATGAGGTGTACTCGGCTGCGATGAGTGTCTTCTGACCTGCTCATC 300	241 CGGCGCACGCTGATGAGGTGTACTCGGCTGCGATGAGTGTCTTCTGACCTGCTCATC 300			
241 CGGCGCACGCTGATGAGGTGTACTCGGCTGCGATGAGTGTCTTCTGACCTGCTCATC 300	241 CGGCGCACGCTGATGAGGTGTACTCGGCTGCGATGAGTGTCTTCTGACCTGCTCATC 300			
301 GTGCACTGTGCGGCATCAGCGCTGAGACCGGCTGAGCCGCGCGCTGAGATAC 360	301 GTGCACTGTGCGGCATCAGCGCTGAGACCGGCTGAGCCGCGCGCTGAGATAC 360			
301 GTGCACTGTGCGGCATCAGCGCTGAGACCGGCTGAGCCGCGCGCTGAGATAC 360	301 GTGCACTGTGCGGCATCAGCGCTGAGACCGGCTGAGCCGCGCGCTGAGATAC 360			
361 AACTTCGAAGCGCACCCCGCGCGCATGAGTGCATCTCTCACTGTGTGCTCATGCGC 420	361 AACTTCGAAGCGCACCCCGCGCGCATGAGTGCATCTCTCACTGTGTGCTCATGCGC 420			
361 AACTTCGAAGCGCACCCCGCGCGCATGAGTGCATCTCTCACTGTGTGCTCATGCGC 420	361 AACTTCGAAGCGCACCCCGCGCGCATGAGTGCATCTCTCACTGTGTGCTCATGCGC 420			
421 GCGGTGATCTGCTGCGCGCCCTCATATCAAGGCGGCAAGAGGCGCGCGCGG 480	421 GCGGTGATCTGCTGCGCGCCCTCATATCAAGGCGGCAAGAGGCGCGCGCGG 480			
421 GCGGTGATCTGCTGCGCGCCCTCATATCAAGGCGGCAAGAGGCGCGCGCGG 480	421 GCGGTGATCTGCTGCGCGCCCTCATATCAAGGCGGCAAGAGGCGCGCGCGG 480			
481 CGCCCCAAGTGAAGCTCAACCAAGAGGCGCTGTGATCTCTGAGCTTCAGCATCGATCT 540	481 CGCCCCAAGTGAAGCTCAACCAAGAGGCGCTGTGATCTCTGAGCTTCAGCATCGATCT 540			
481 CGCCCCAAGTGAAGCTCAACCAAGAGGCGCTGTGATCTCTGAGCTTCAGCATCGATCT 540	481 CGCCCCAAGTGAAGCTCAACCAAGAGGCGCTGTGATCTCTGAGCTTCAGCATCGATCT 540			
541 TTCTTTGCTCGTGGCGCATATGATCTCTGCTGCTGCTGAGCTTCACTGATCGCCAAA 600	541 TTCTTTGCTCGTGGCGCATATGATCTCTGCTGCTGCTGAGCTTCACTGATCGCCAAA 600			
541 TTCTTTGCTCGTGGCGCATATGATCTCTGCTGCTGCTGAGCTTCACTGATCGCCAAA 600	541 TTCTTTGCTCGTGGCGCATATGATCTCTGCTGCTGCTGAGCTTCACTGATCGCCAAA 600			
601 CGAGCAACCGCAGAGGTCCCAAGGCGCAAGGCGGCGCTGTGAGGAGTGTCAAGCAG 660	601 CGAGCAACCGCAGAGGTCCCAAGGCGCAAGGCGGCGCTGTGAGGAGTGTCAAGCAG 660			
601 CGAGCAACCGCAGAGGTCCCAAGGCGCAAGGCGGCGCTGTGAGGAGTGTCAAGCAG 660	601 CGAGCAACCGCAGAGGTCCCAAGGCGCAAGGCGGCGCTGTGAGGAGTGTCAAGCAG 660			
661 CCGGACCCGACCATGATGAGGCTTTTGGCTCAGCCAACTGCGACGCTGTGCTGTG 720	661 CCGGACCCGACCATGATGAGGCTTTTGGCTCAGCCAACTGCGACGCTGTGCTGTG 720			
661 CCGGACCCGACCATGATGAGGCTTTTGGCTCAGCCAACTGCGACGCTGTGCTGTG 720	661 CCGGACCCGACCATGATGAGGCTTTTGGCTCAGCCAACTGCGACGCTGTGCTGTG 720			

QY 721 GCTTCTGCCAGAGAGTCAACGACACTCGAAGTCCACTGGGAGAGAGAGGAGGAG 780
DB 721 GCTTCTGCCAGAGAGTCAACGACACTCGAAGTCCACTGGGAGAGAGAGGAGGAG 780
QY 781 ACCCTGGAAGATCTGGGAGACCCGGGCTTGGCCACCAAGTTGGGCTCCCTCCAACTCA 840
DB 781 ACCCTGGAAGATCTGGGAGACCCGGGCTTGGCCACCAAGTTGGGCTCCCTCCAACTCA 840
QY 841 GGCAGAGGCGCAGAGAGAGGAGTGTGTGTGGGCGATCTCCAGAGATGAAGTGAAGAGAG 900
DB 841 GGCAGAGGCGCAGAGAGAGGAGTGTGTGTGGGCGATCTCCAGAGATGAAGTGAAGAGAG 900
QY 901 GAAAGAGAGAGAGAGAGAG 918
DB 901 GAAAGAGAGAGAGAGAGAG 918

RESULT 8
AA199906
ID AA199906 standard; DNA; 1344 BP.
XX
AC AA199906;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; db.
XX
OS Homo sapiens.

XX
XX Key Location/Qualifiers
FH 1..1344
FT /tag= a
FT /product= "alpha-2BAR"
FT /note= "sequence is deleted for a 9 nucleotide
FT polymorphic site found at nucleotides 901-909
FT of the wildtype alpha-2BAR protein (AA199905)"
PN MO200179561-A2.
XX
PD 25-OCT-2001.
XX
XX 17-APR-2001; 2001MO-US12575.
XX PF
XX 17-APR-2000; 2000US-0551744.
XX PR
XX 10-AUG-2000; 2000US-0636259.
XX PR
XX 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
XX PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
XX WPI; 2001-611728/70.
XX DR P-PSDB; AAMS2118.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
XX disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
XX
XX Claim 5; Page 144-145; 163pp; English.

CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909

CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (ggggcggggcgc) or (B) (ggggcggcgcag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlates to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHR933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the third intracellular loop of
CC the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
CC polymorphic site found at nucleotides 901-909 of the wildtype gene
CC (AA199905).
XX
XX Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;
XX

Query Match 66.7%; Score 902; DB 23; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGACACAG 60
DB 1 ATGAGACACAG 60
QY 61 TTCTCATCTCTCTTACATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 61 TTCTCATCTCTTACATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 CGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 121 CGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 181 GTGGCAG 240
DB 181 GTGGCAG 240
QY 241 CGGCGAG 300
DB 241 CGGCGAG 300
QY 301 GTGCACTGTGCGGAG 360
DB 301 GTGCACTGTGCGGAG 360
QY 361 AACTCAG 420
DB 361 AACTCAG 420
QY 421 GCGTCATCTGCGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 421 GCGTCATCTGCGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
QY 481 CGGCGGAG 540
DB 481 CGGCGGAG 540
QY 541 TTCTTTGCTCTGCTGCTCATCATCATCTTGTCTACCTGCGAGATCACTGATCGCAAA 600
DB 541 TTCTTTGCTCTGCTGCTCATCATCATCTTGTCTACCTGCGAGATCACTGATCGCAAA 600
QY 601 CGCAG 660
DB 601 CGCAG 660
QY 661 CCCGAG 720
DB 661 CCCGAG 720

Db 661 CCCGACCCGACCATGTTGGGGCTTTGGCTTCAGCCAACTGCGACCCCTGGCTCTGTG 720
QY 721 GCTTCTCCAGAGAGGTCAACGGAGCACTGAACTCACTGGAGAGAGAGGGGGAG 780
Db 722 GCTTCTCCAGAGAGGTCAACGGAGCACTGAACTCACTGGAGAGAGAGGGGGAG 780
QY 781 ACCCTGAAGATACCTGGGACCCGGGCTTGGCAACCAAGTTGGGCTGCTTCCAACTCA 840
Db 781 ACCCTGAAGATACCTGGGACCCGGGCTTGGCAACCAAGTTGGGCTGCTTCCAACTCA 840
QY 841 GGGCAGGGCCAGAGAGGCTTTTGGGGGCACTCCAGAGATGAGCTGAGAGAGAG 900
Db 841 GGGCAGGGCCAGAGAGGCTTTTGGGGGCACTCCAGAGATGAGCTGAGAGAGAG 900
QY 901 GA 902
Db 901 GA 902
Db 901 GA 902

RESULT 9

AAQ14151 standard; DNA; 2064 BP.

XX AAQ14151;
XX AC
XX AAQ14151;
XX 06-JAN-1992 (first entry)
XX Human alpha 2 beta adrenergic receptor gene.
XX Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
XX Homo. sapiens.
XX OS
XX Key Location/Qualifiers
XX FT CDS 288..1752
XX FT /*tag= a
XX FT
XX US5053337-A.
XX PN 01-OCT-1991.
XX PD 30-OCT-1989; 89US-0428856.
XX PF 30-OCT-1989; 89US-0428856.
XX PR 30-OCT-1989; 89US-0428856.
XX PA (NEUR-) NEUROGENETIC CORP.
XX PI Weishank RL, Hartig PR;
XX DR WPI; 1991-310087/42.
XX DR P-PSDB; AARI1419.
XX PT Isolated DNA encoding human adrenergic receptor - for detecting
XX PT nucleic acids encoding alpha, 2-beta adrenergic receptor, for
XX PT screening drugs.
XX PS Claim 1; Fig 2; 15BP; English.
XX CC Clone NGC-alpha2beta was isolated from a human spleen genomic
XX CC library by screening with a fragment of the human 5-HT1A receptor
XX CC gene. The gene can be used to express recombinant receptor protein
XX CC which can be used to produce antibodies for inhibition of receptor
XX CC function.
XX SQ Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;

Query Match

60.6%; Score 820; DB 12; Length 2064;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 970; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 381 CCGCATCAAGTGCATATCTCACTGTGTGGCTCATCGCCGCGCATCTGGCTGCGGC 440
Db 779 CCGCATCAAGTGCATATCTCACTGTGTGGCTCATCGCCGCGCATCTGGCTGCGGC 838

QY 441 CTTATCTCAAGAGGAGCAAGAGGCCCCAGCGCGCGGCGCCCCAGTGCAGACTCA 500
Db 839 CTTATCTCAAGAGGAGCAAGAGGCCCCAGCGCGCGGCGCCCCAGTGCAGACTCA 898
QY 501 CCAAGAGGCTGTGTACATCTGTGCTTCAGCATCTGATCTTTTGTGCTTGTGCTCAT 560
Db 899 CCAAGAGGCTGTGTACATCTGTGCTTCAGCATCTGATCTTTTGTGCTTGTGCTCAT 958
QY 561 CATGATCTTGTGTACCTGTGCACTTACCTGATGCGCAACGAGAGCAACGAGAGTCC 620
Db 959 CATGATCTTGTGTACCTGTGCACTTACCTGATGCGCAACGAGAGCAACGAGAGTCC 1018
QY 621 CAGGGCCAAAGGGGGGCTGCGGAGAGTGAAGTCAAGACCCCGACCCGACCATGTTG 680
Db 1019 CAGGGCCAAAGGGGGGCTGCGGAGAGTGAAGTCAAGACCCCGACCCGACCATGTTG 1078
QY 681 GGGTTTGGCTCAGCCAAACTGCGAGCCCTGGGCTCTGTGGCTTCTGCGAGAGTCAA 740
Db 1079 GGGTTTGGCTCAGCCAAACTGCGAGCCCTGGGCTCTGTGGCTTCTGCGAGAGTCAA 1138
QY 741 CCGACACTCGAAGTCACTGGGGAGAGAGAGGGGAGACCCCTGAAGATCTGGGAC 800
Db 1139 CCGACACTCGAAGTCACTGGGGAGAGAGAGGGGAGACCCCTGAAGATCTGGGAC 1198
QY 801 CCGGCTTGTGCAACCTGAGTGGCTGCTTCCCACTCAGGCGCAGAGGCGAGAGAGG 860
Db 1199 CCGGCTTGTGCAACCTGAGTGGCTGCTTCCCACTCAGGCGCAGAGGCGAGAGAGG 1258
QY 861 TGTTTTGGGGCATCTCCAGAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAG 920
Db 1259 TGTTTTGGGGCATCTCCAGAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAG 1318
QY 921 GGAAGAGTGAACCCAGAGAGTGCAGTGTCTCCGCTCAGCTTGACCCCGGCT 980
Db 1319 GGAAGAGTGAACCCAGAGAGTGCAGTGTCTCCGCTCAGCTTGACCCCGGCT 1378
QY 981 GCAGAGCCCAAGGCTCCCGGCTGCTGGCCACCTTACGAGAGGCTCTGGGAG 1040
Db 1379 GCAGAGCCCAAGGCTCCCGGCTGCTGGCCACCTTACGAGAGGCTCTGGGAG 1438
QY 1041 GGGCGTGGGTGCTATAGGTGGGCAAGTGTGCTGAGAGGCGAGCTGACCCGGAGAA 1100
Db 1439 GGGCGTGGGTGCTATAGGTGGGCAAGTGTGCTGAGAGGCGAGCTGACCCGGAGAA 1498
QY 1101 GCGCTTCACTTCTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160
Db 1499 GCGCTTCACTTCTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1558
QY 1161 CTTCTTCACTTCTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1220
Db 1559 CTTCTTCACTTCTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1618
QY 1221 CTTCAAGTCTTCTTGTGATCGGCTACTGCAACAGCTCACTGAACCTGTTATCTAC 1280
Db 1619 CTTCAAGTCTTCTTGTGATCGGCTACTGCAACAGCTCACTGAACCTGTTATCTAC 1678
QY 1281 CATCTTCAACGAGACTTCCCGCTGCTTCCGAGAGAGCTGTGCGCGCGTGAACCA 1340
Db 1679 CATCTTCAACGAGACTTCCCGCTGCTTCCGAGAGAGCTGTGCGCGCGTGAACCA 1738
QY 1341 GAGGCTGTGCTGA 1353
Db 1739 GAGGCTGTGCTGA 1751

RESULT 10

AAT59499 standard; DNA; 2064 BP.

AAT59499;

DT 25-MAR-2003 (updated)

DT 06-MAY-1997 (first entry)
XX Human alpha-2b adrenergic receptor genomic DNA clone.
DE Alpha-2b adrenergic receptor; adrenoreceptor; adrenaline;
XX epinephrine; signal transduction; neurotransmitter; ligand; ss.
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
FT CDS 288..1751
FT /-tag= a
XX
XX US595880-A.
XX
XX 21-JAN-1997.
XX
XX 22-OCT-1992; 92US-0965040.
XX
XX 30-OCT-1989; 89US-0428856.
XX 30-MAY-1991; 91US-0707604.
XX 22-OCT-1992; 92US-0965040.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX
XX Hartig PR, Weisshank RL;
XX
XX WPI: 1997-107576/10.
XX P-PSDB; AAM11804.
XX
XX Assay for alpha-2b adrenergic receptor ligands - using membranes of
XX cells expressing recombinant receptor
XX
XX Disclosure; Fig 2A-E; 16pp; English.
XX
XX A genomic DNA clone (AAT59499) codes for human alpha-2b adrenergic
XX receptor (AAM11804), a member of the rhodopsin-like signal transducer
XX family. It was isolated from a human spleen genomic library in the
XX lambda vector Charon 28 by screening with a 1.6 kb fragment of the
XX human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2b
XX comprising DNA encoding the alpha-2b adrenoreceptor is deposited as
XX ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2b
XX adrenoreceptor in bacterial, yeast or mammalian cells; transfected
XX Lck- cells, designated L-NGC-alpha-2b, are deposited as ATCC CRL
XX 10275. Membranes of such cells can used in novel methods to
XX identify drugs which specifically interact with, and bind to, the
XX alpha-2b adrenergic receptor.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
SQ

Query Match 60.6%; Score 820; DB 18; Length 2064;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 381 CGGCATCAAGTGCATGATCTCACTGTCGCTCATCGCGCGCTGCTGCGCGC 440
DB 779 CGGCATCAAGTGCATGATCTCACTGTCGCTCATCGCGCGCTGCTGCGCGC 838
QY 441 CCTCATCTCAAGAGGCGACGAGGCGCCCGAGCGCGCGCGCGCGCGCGCGCTCA 500
DB 839 CCTCATCTCAAGAGGCGACGAGGCGCCCGAGCGCGCGCGCGCGCGCGCGCTCA 898
QY 501 CCAAGAGGCGCTGTCATCTGCGCTCCAGCATCGGATCTTTCTTGTCTCTGCTCAT 560
DB 899 CCAAGAGGCGCTGTCATCTGCGCTCCAGCATCGGATCTTTCTTGTCTCTGCTCAT 958
QY 561 CATGATCTTGTCTACCTGCGGATCTTACCTGATCGCAAGCAAGCAAGCAAGAGTCC 620
DB 959 CATGATCTTGTCTACCTGCGGATCTTACCTGATCGCAAGCAAGCAAGCAAGAGTCC 1018
QY 621 CAGGCGCAAGGAGGCGCTGCGGAGGTGATCCAGCAAGCCCGCAAGCATGCTG 680

DB 1019 CAGGCGCAAGGAGGCGCTGCGGAGGTGATCCAGCAAGCCCGCAAGCATGCTG 1078
QY 681 GGCCTTGACCTCAGCAAGTGCAGGCGCTGCGCTGTCGCTTCTGCGAGAGGTCA 740
DB 1079 GGCCTTGACCTCAGCAAGTGCAGGCGCTGCGCTGTCGCTTCTGCGAGAGGTCA 1138
QY 741 CCGACACTGCAAGTGCAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 800
DB 1139 CCGACACTGCAAGTGCAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1198
QY 801 CCGGCGCTTGCCAGCCAGTGGCTGCTCCCTTCCCACTAGGCGAGGCGCAAGAGAGG 860
DB 1199 CCGGCGCTTGCCAGCCAGTGGCTGCTCCCTTCCCACTAGGCGAGGCGAGAGAGG 1258
QY 861 TGTGTGGGGGATCTCCAGAGATGAGCTGAGAGGAGAGAGAGAGAGAGAGAGG 920
DB 1259 TGTGTGGGGGATCTCCAGAGATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGG 1318
QY 921 GGAAGAGTGAACCCAGGAGTGCAGTGTCTCCGCGCTCAGCTTGAGGCCCGCGCT 980
DB 1319 GGAAGAGTGAACCCAGGAGTGCAGTGTCTCCGCGCTCAGCTTGAGGCCCGCGCT 1378
QY 981 GCAAGAGCCACAGGCGCTCCCGGCTGCGCACCTTACCTGCGAGTGTCTCTGCGCAG 1040
DB 1379 GCAAGAGCCACAGGCGCTCCCGGCTGCGCACCTTACCTGCGAGTGTCTCTGCGCAG 1438
QY 1041 GGGCGTGGGTATATAGTGGGAGTGGGAGTGGAGGAGGAGGAGGAGGAGGAGG 1100
DB 1439 GGGCGTGGGTATATAGTGGGAGTGGGAGTGGAGGAGGAGGAGGAGGAGGAGG 1498
QY 1101 GGGCTTACCTTCTGTCGCTGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCT 1160
DB 1499 GGGCTTACCTTCTGTCGCTGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCT 1558
QY 1161 CTCTTCACTCAAGCTGCGCGCATCTGCGCGCACTGCGCAAGTGCAGGCGCT 1220
DB 1559 CTCTTCACTCAAGCTGCGCGCATCTGCGCGCACTGCGCAAGTGCAGGCGCT 1618
QY 1221 CTCTTCACTTCTTCTGATGCGCTACCTGCAAGCTGCAAGCTGCAAGCTGCAAG 1280
DB 1619 CTCTTCACTTCTTCTGATGCGCTACCTGCAAGCTGCAAGCTGCAAGCTGCAAG 1678
QY 1281 CATCTTCAACAGACTTCCGCGCTTCCGAGAGATCTGTCGCGCGCGCGCGCA 1340
DB 1679 CATCTTCAACAGACTTCCGCGCTTCCGAGAGATCTGTCGCGCGCGCGCGCA 1738
QY 1341 GACGCGCTGCTGA 1353
DB 1739 GACGCGCTGCTGA 1751

RESULT 11
ABN32100
ID ABN32100 standard; DNA; 65 BP.
XX
XX ABN32100;
XX
XX 15-JUL-2002 (first entry)
XX
XX
XX Rat spliced transcript detection oligonucleotide SEQ ID NO:4848.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Rattus norvegicus.
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-1B01903.
XX
XX 28-JUL-2000; 2000US-221607P.
XX


```

FH Key Location/Qualifiers
FT CDS 1..1353
FT /*tag= a
FT /product= "alpha-2AAR"
XX
XX WO200179561-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12575.
XX
XX 17-APR-2000; 2000US-0551744.
XX 10-AUG-2000; 2000US-0636259.
XX 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
XX (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
XX WPI: 2001-611728/70.
XX P-PSDB; AAMS2122.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
XX disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
XX
XX Example 7, Page 151; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX alpha2A or alpha2C or fragment or complement of; and
XX (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX of (I), a site comprising cytosine or guanine at position 753 of (IIV)
XX or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at
XX positions 961-972 of (III). The method may be used for genotyping an
XX alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX whether an individual is at increased risk of developing a disease
XX associated with alpha2B, alpha2A or alpha2, comprising detecting a
XX polymorphic site which correlate to disease selected from cardiovascular
XX disease, central nervous system disease and combinations of these. In
XX addition, the technique may be used to predict an individual's response
XX to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, BHT933 and
XX norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX rauwolficine, idazoxan, tolazoline, phentolamine and combinations of
XX these) by detecting the polymorphic site and correlating the site to a
XX predetermined response (where the response is correlated to adenylyl
XX cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX levels). The present sequence is that of the human alpha-2AAR gene
XX (Genbank Accession AF281308).
XX
XX Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;
XX
XX Query Match 3.3%; Score 45; DB 23; Length 1350;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-10;
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 292 TCGTCATCGTGCACCTGTGGCCATCAGCTGACCGCTACTG 336
XX |||||||||||||||||||||||||||||||||||||||
XX 355 TCGTCATCGTGCACCTGTGGCCATCAGCTGACCGCTACTG 399
XX
XX RESULT 14
XX AA199918
XX ID AA199918 standard; DNA; 1350 BP.
XX AC AA199918;
XX XX
XX 18-FEB-2002 (first entry)
XX
```

```

DE Human alpha-2AAR variant encoding DNA.
XX
XX Human: genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX polymorphic site; allelic variant; cardiovascular disease;
XX central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1353
XX /*tag= a
XX /product= "alpha-2AAR"
XX replace(753,C)
XX /*tag= b
XX
XX WO200179561-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12575.
XX
XX 17-APR-2000; 2000US-0551744.
XX 10-AUG-2000; 2000US-0636259.
XX 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
XX (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
XX WPI: 2001-611728/70.
XX P-PSDB; AAMS2123.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
XX disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
XX
XX disclosure; Page 152; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX alpha2A or alpha2C or fragment or complement of; and
XX (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX of (I), a site comprising cytosine or guanine at position 753 of (IIV)
XX or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at
XX positions 961-972 of (III). The method may be used for genotyping an
XX alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX whether an individual is at increased risk of developing a disease
XX associated with alpha2B, alpha2A or alpha2, comprising detecting a
XX polymorphic site which correlate to disease selected from cardiovascular
XX disease, central nervous system disease and combinations of these. In
XX addition, the technique may be used to predict an individual's response
XX to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
XX norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX rauwolficine, idazoxan, tolazoline, phentolamine and combinations of
XX these) by detecting the polymorphic site and correlating the site to a
XX predetermined response (where the response is correlated to adenylyl
XX cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX levels). The present sequence is that of the human alpha-2AAR variant
XX gene.
XX
XX Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
XX
XX Query Match 3.3%; Score 45; DB 23; Length 1350;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-10;
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 292 TCGTCATCGTGCACCTGTGGCCATCAGCTGACCGCTACTG 336
XX |||||||||||||||||||||||||||||||||||||||
XX
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DB 355 TCGTCATCGTGACCTGTGGCCATCAGCTGACCGCTACTGG 399

Search completed: February 8, 2004, 01:59:37
Job time : 402.321 secs

RESULT 15

ACAS6582
ID ACAS6582 standard; cDNA; 3604 BP.

AC ACAS6582;

DT 06-JUN-2003 (first entry)

DE Human signalling pathway polynucleotide probe SEQ ID NO 1180.

KW Human; Probe; ss; array element; Parkinson's disease;

KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

OS Homo sapiens.

PN US6500938-B1.

PD 31-DEC-2002.

PF 30-JAN-1998; 98US-0016434.

PR 30-JAN-1998; 98US-0016434.

PA (INCY-) INCYTE GENOMICS INC.

PI Au-Young J, Sellhammer JJ;

DR WPI; 2003-352169/33.

PT Combination of polynucleotide probes, useful as array elements in a

PT microarray for monitoring the expression of a number of target

PS Claim 1; SEQ ID NO 1180; 65bp; English.

CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostic and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signalling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docID=06500938B1.

XX Sequence 3604 BP; 555 A; 1272 C; 1134 G; 643 T; 0 other;

Query Match 3.3%; Score 45; DB 25; Length 3604;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCGTCATCGTGACCTGTGGCCATCAGCTGACCGCTACTGG 336
DB 2432 TCGTCATCGTGACCTGTGGCCATCAGCTGACCGCTACTGG 2476


```

QY 601 CGCAGCAACCGCAGAGGCTCCAGGGGCCAAAGGGGGGGGGCTGGGCGAGGGGAGTCCAAACG 660
Db 1013 CGCAGCAACCGCAGAGGCTCCAGGGGCCAAAGGGGGGGGGCTGGGCGAGGGTGAATCCAAACG 1072
QY 661 CCGCAGCCCGACCAATGATGAGGGCTTTGGGCTTCAGCCAACTGCCAGCCCTGGCTGTG 720
Db 1073 CCGCAGCCCGACCAATGATGAGGGCTTTGGGCTTCAGCCAACTGCCAGCCCTGGCTGTG 1132
QY 721 GCTTCTGCAGAGAGGTCAACGACACTTCGAAGTCACTGGGGGAGAGAGAGAGGGGAG 780
Db 1133 GCTTCTGCAGAGAGGTCAACGACACTTCGAAGTCACTGGGGGAGAGAGAGAGGGGAG 1192
QY 781 ACCCTGAAAGATCTGGGAGCCCGGGCTTGGCAACCGAGTTGGGGGCGCCCTTCCCACTCA 840
Db 1193 ACCCTGAAAGATCTGGGAGCCCGGGCTTGGCAACCGAGTTGGGGGCGCCCTTCCCACTCA 1252
QY 841 GCGCAGGAGCCAGAAAGAGAGGATGTTGTGTGGGCATCTCCAGAGATGAAGCTGAAGAGAG 900
Db 1253 GCGCAGGAGCCAGAAAGAGAGGATGTTGTGTGGGCATCTCCAGAGATGAAGAGAGAG 1312
QY 901 GAAAGAGAGAGAGAGAGAGAGAGAGATGTGAACCCAGGCAATGTCAGTGTCTTCGGCC 960
Db 1313 GAAAGAGAGAGAGAGAGAGAGAGAGATGTGAACCCAGGCAATGTCAGTGTCTTCGGCC 1372
QY 961 TCAGCTTTCAGAGCCCCCGGCTGAGAGGCAACAGGGCTCCGGGGTGTGGCCACCCCTACGT 1020
Db 1373 TCAGCTTTCAGAGCCCCCGGCTGAGAGGCAACAGGGCTCCGGGGTGTGGCCACCCCTACGT 1432
QY 1021 GGCACAGTGTCTCTGGGCGAGGGGCGTGGGATGCTAAGGTGGGACAGTGTGGCGTTCGAAG 1080
Db 1433 GGCACAGTGTCTCTGGGCGAGGGGCGTGGGATGCTAAGGTGGGACAGTGTGGCGTTCGAAG 1492
QY 1081 GCGCAGCTGACCCCGGAGAGAGCGCTTCAACCTTCTGTGGCTGTGTGTATTGGGGTTTT 1140
Db 1493 GCGCAGCTGACCCCGGAGAGAGCGCTTCAACCTTCTGTGGCTGTGTGTATTGGGGTTTT 1552
QY 1141 GTGCTCTGTGTGTTCCTCTTCTTTTCAGCTACAGCCTGGGGCGCATCTGGCCGAGAC 1200
Db 1553 GTGCTCTGTGTGTTCCTCTTCTTTTCAGCTACAGCCTGGGGCGCATCTGGCCGAGAC 1612
QY 1201 TGCAGAGTGCCCCCATGGGCTCTTCAGATTCTTCTTGGATCGGCTACTGCAACAGCTCA 1260
Db 1613 TGCAGAGTGCCCCCATGGGCTCTTCAGATTCTTCTTGGATCGGCTACTGCAACAGCTCA 1672
QY 1261 CTGAACCCCTGTATCTACACATCTTCAACAGAGCTTCCGCGGTGCTTCCGAGAGATC 1320
Db 1673 CTGAACCCCTGTATCTACACATCTTCAACAGAGCTTCCGCGGTGCTTCCGAGAGATC 1732
QY 1321 CTGTGCGGCGCGGTGAGACCCAGACGGCGCTGTGA 1353
Db 1733 CTGTGCGGCGCGGTGAGACCCAGACGGCGCTGTGA 1765

RESULT 2
US-09-016-434-1180
/ Sequence 1180, Application US/09016434
/ Patent No. 6500938
/ GENERAL INFORMATION:
/ APPLICANT: Janice Au-Young
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
/ TITLE OF INVENTION: PATHWAY GENE EXPRESSION
/ NUMBER OF SEQUENCES: 1490
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/

```

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016.434
 FILING DATE: HEREMITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37, 071
 REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1180:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3604 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g178195
 US-09-016-434-1180

Query Match 3.3%; Score 45; DB 4; Length 3604;
 Best Local Similarity 100.0%; Pred. No. 6.3e-11;
 Matches 45; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

RESULT 3
 US-09-016-434-1256
 Sequence 1256, Application US/09016434
 Patent No. 6500938
 GENERAL INFORMATION:
 APPLICANT: Janice Au-Young
 APPLICANT: Jeffrey J. Sellhammer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,434
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2004, 01:25:52 / Search time 3134.43 Seconds
(without alignments)
10491.225 Million cell updates/sec

Title: US-09-692-077D-1

Perfect score: 1353
Sequence: 1 atgagaccaccagaccctca.....ggagccagacgagcctcgtca 1353

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 30

Total number of hits satisfying chosen parameters: 193

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Listing first 45 summaries

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EST:
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29: em_estbda:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	28.4	1044	BQ880026	BQ880026 AGENCOURT
2	47	3.5	551	A1169366	A1169366 EST215210
3	47	3.5	731	CA511027	CA511027 UI-R-FJO-
4	45	3.3	2410	BC035047	BC035047 Homo sapi

5	44	3.3	893	12	B1459381	B1459381 603200147
6	41	3.0	872	29	EC0A2BAR	EC0A2BAR 603200147
7	39	2.9	301	14	T39448	T39448 y406a09.r2
8	39	2.9	978	13	B0539106	B0539106 AGENCOURT
9	39	2.9	1031	13	B0538114	B0538114 AGENCOURT
10	39	2.9	1176	9	AL549866	AL549866 AL549866
11	39	2.9	1201	9	AL573897	AL573897 AL573897
12	38	2.8	988	13	BQ887729	BQ887729 AGENCOURT
13	36	2.7	256	14	CA315228	CA315228 UI-M-FW0-
14	36	2.7	1000	12	BG915999	BG915999 602815267
15	35	2.6	578	14	CA752540	CA752540 UI-M-FW0-
16	35	2.6	716	28	AZ286027	AZ286027 RPCT-23-1
17	35	2.6	826	29	BZ227940	BZ227940 CH230-400
18	34	2.5	683	12	BG830756	BG830756 602767450
19	34	2.5	855	29	CGA42AAR	CGA42AAR Chicken a
20	34	2.5	960	13	B0538113	B0538113 AGENCOURT
21	34	2.5	967	29	CNS03THX	CNS03THX Tetraodon
22	33	2.4	253	28	AZ632452	AZ632452 Tetraodon
23	33	2.4	271	10	BE762670	BE762670 RC3-NT001
24	33	2.4	290	14	CD553892	CD553892 B0367B12-
25	33	2.4	295	28	AZ497396	AZ497396 IM0334B18
26	33	2.4	348	28	A0638574	A0638574 927P1-12C
27	33	2.4	385	28	BH041461	BH041461 RPCT-24-3
28	33	2.4	416	10	BB677036	BB677036 BB677036
29	33	2.4	418	29	BZ248154	BZ248154 CH230-498
30	33	2.4	426	29	BZ232448	BZ232448 CH230-427
31	33	2.4	430	28	AZ223727	AZ223727 RPCT-23-6
32	33	2.4	451	9	A1461341	A1461341 fb43d01.x
33	33	2.4	483	14	BT710352	BT710352 BT710352
34	33	2.4	485	14	CD553443	CD553443 B0359G11-
35	33	2.4	568	29	TA161D03P	TA161D03P T. brucei
36	33	2.4	573	12	B0037704	B0037704 PgmC.DK0
37	33	2.4	600	28	AZ653623	AZ653623 IM0527E24
38	33	2.4	672	10	BB262531	BB262531 BB262531
39	33	2.4	713	28	AZ288043	AZ288043 RPCT-23-1
40	33	2.4	860	29	CNS03HQK	CNS03HQK Tetraodon
41	33	2.4	887	12	BT734330	BT734330 60351261
42	33	2.4	1101	29	CNS052LD	AL118298 Tetraodon
43	33	2.4	2758	11	AK004657	AK004657 Mus muscu
44	32	2.4	167	28	BH072396	BH072396 RPCT-24-2
45	32	2.4	350	10	BB648878	BB648878 UI-M-BH2.

ALIGNMENTS

RESULT 1
BQ880026
LOCUS
DEFINITION
AGENCOURT 813358 lupski dorsal root ganglion Homo sapiens cDNA
clone IMAGE:617905 5', mRNA sequence.
BQ880026
VERSION
BQ880026.1 GI:22272034
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1044)
NHI-MGC http://mgc.nci.nih.gov/
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LILN at:
http://image.llnl.gov
plate: LILN1359 row: 1 column: 20
High quality sequence stop: 430.

FEATURES
source

Seq primer: M13 REVERSE.
Location/Qualifiers

1. 731
/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-FJ0-cpv-h-10-0-UI"

/issue_type="embryo"

/dev_stage="embryo"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_1ib="UI-R-FJ0"

/note="Vector: pX-Asc; Site 1: EcoR I; Site 2: Not I;

UI-R-FJ0 is a cDNA library containing the following

tissue(s): rat embryo. The library was constructed

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT73-Pac

vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The

sequence tag for this library is CATCTCTACT. This library

was created for the University of Iowa Program for Rat

Gene Discovery and Mapping (Val Sheffield, Bento Soares

and Tom Casavant)"

BASE COUNT 128 a 217 c 163 g 223 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 47; DB 14; Length 731;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1213 CATGCCCTCTTCAGTCTTCTTCGATCGCTACTGCAACGCTC 1259

Db 42 CATGCCCTCTTCAGTCTTCTTCGATCGCTACTGCAACGCTC 88

RESULT 4 BC035047 2410 bp mRNA 1linear HTC 23-SEP-2002

LOCUS Homo sapiens, Similar to adrenergic, alpha-2A-, receptor, clone

IMAGE:5266354, mRNA.

ACCESSION BC035047.1 GI:23272892

VERSION HTc.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 2410)

Strausberg, R.

Direct Submission

Submitted (31-JUL-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK

COMMENT

Series: IRAX Plate: 73 Row: 0 Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 15718669
This clone has the following problem: frame shifted.

Location/Qualifiers

1. 2410

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5266354"

/issue_type="Testis"

/clone_1ib="NIH_MGC_97"

/lab_host="DH10B"

/note="Vector: pBluescript"

BASE COUNT 406 a 813 c 721 g 470 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 45; DB 11; Length 2410;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TCGTCATGTCGACCTGCGCCATACGCTGACCGCTACTGG 336

Db 568 TCGTCATGTCGACCTGCGCCATACGCTGACCGCTACTGG 612

RESULT 5 BI459381 893 bp mRNA 1linear EST 21-AUG-2001

LOCUS 603200147F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266354 5',

ACCESSION BI459381 mRNA sequence.

VERSION BI459381.1 GI:15250037

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 893)

NIH-MGC <http://mgc.nci.nih.gov/>.

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Miklos Palokovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM11671 row: m column: 11

High quality sequence stop: 716.

Location/Qualifiers

1. 893

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5266354"

/lab_host="DH10B"

/clone_1ib="NIH_MGC_97"

/note="Organ: testis; Vector: pBluescript (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (Gcgag

) ; Oligo-dT primed using primer 5'-TTTTTTTTTTTAA-3',

size-selected for average insert size 2.2 kb and

normalized to 10^5. This is a primary library enriched

for full-length clones and constructed using the

cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NHGRI, National

Institutes of Health). Note: this is a NIH_MGC library."

BASE COUNT

ORIGIN

149 a

303 c

290 g

151 t

Query Match 3.3%; Score 44; DB 12; Length 893;
 Best Local Similarity 100.0%; Pred. No. 4.3e-09;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 CGTCATCGTGCACCTGTGGCCATCAGCGCTGACCGTACTG 336
 574 CGTCATCGTGCACCTGTGGCCATCAGCGCTGACCGTACTG 617

RESULT 6
 ECMA2BAR 872 bp DNA linear GSS 14-SEP-2001
 LOCUS Horse alpha2 adrenergic receptor gene fragment probably subtype b,
 DEFINITION genomic survey sequence.
 ACCESSION AL606560
 VERSION AL606560.1 GI:15591917
 KEYWORDS GSS; Alpha2 adrenergic receptor gene.
 SOURCE Equus caballus (horse)
 ORGANISM Equus caballus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 1 (bases 1 to 872)
 Hunter, C. and Elgar, G.
 Alpha2 adrenergic receptor gene
 Unpublished
 2 (bases 1 to 872)
 Hunter, C.
 Direct Submission
 Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB. UK Email:
 biohel@hmp.mrc.ac.uk
 Location/Qualifiers
 1..872
 /organism="Equus caballus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9796"

BASE COUNT 156 a 277 c 280 g 159 t

ORIGIN

Query Match 3.0%; Score 41; DB 29; Length 872;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 553 TGCCATCATCATGATCTGTCTACCTGCGCATCTACTGAT 593
 244 TGCCATCATCATGATCTGTCTACCTGCGCATCTACTGAT 284

RESULT 7
 LOCUS 301 bp mRNA linear EST 27-JAN-1995
 DEFINITION y006a09.2 Stragene placenta (#937225) Homo sapiens cDNA clone
 IMAGE:60664 5' similar to SP:AZAD_HUMAN P35369
 ALPBA-2C-2 ADRENERGIC mRNA sequence.
 ACCESSION T39448.1 GI:647179
 VERSION T39448.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 301)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
 Chissole, S., Dietrich, N., Dubuque, T., Pavello, A., Gib, M., Hawkins
 , M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
 , B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Weg, J., Trevaekis, E.,
 Underwood, K., Woldman, P., Watsen, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 JOURNAL MEDLINE
 PUBMED 8889549

COMMENT Other ESTs: y006a09.61
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: M3RP.

FEATURES
 source
 Location/Qualifiers
 1..301
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:60664"
 /sex="male"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Stragene placenta (#937225)"
 /note="Organ: placenta; Vector: pBluescript SK-; Site 1:
 EcorI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
 XR Vector; ~5' adaptor sequence: 5' GAATTCGACGACG 3' ~3'
 adaptor sequence: 5' CTCGATTTTCTTTTCTTTT 3' ~3"

BASE COUNT 40 a 107 c 71 g 83 t

ORIGIN

Query Match 2.9%; Score 39; DB 14; Length 301;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1141 GTGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1179
 114 GTGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 152

RESULT 8
 LOCUS BUS39106 978 bp mRNA linear EST 13-SEP-2002
 DEFINITION AGNCOURT_10215036 NIH_MGC_107 Homo sapiens cDNA clone
 IMAGE:6559764 5', mRNA sequence.
 ACCESSION BUS39106
 VERSION BUS39106.1 GI:22849547
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 978)
 NIH-MGC http://imgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LNC2757 row: j column: 04
 High quality sequence stop: 554.
 Location/Qualifiers
 1..978
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:6559764"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_107"

FEATURES
 source

100

Email: segreff@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/Invitrogen/Corporation/1600>
Faraday Avenue Genoscope sequence ID : CSDDI054DD01NP1.
Location/Qualifiers

FEATURES

source

1..1201
/organism="Homo sapiens"
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/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NCTI-oligo (GT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 193 a 391 c 364 g 205 t 48 others

ORIGIN

Query Match 2.9%; Score 39; DB 9; Length 1201;
Best Local Similarity 100.0%; Pred. No. 9e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1141 GTGCTGTGCTGCTCCCTCTCTCTGAGCTACGAGCTG 1179
|||||
Db 733 GTGCTGTGCTGCTCCCTCTCTCTGAGCTACGAGCTG 695

RESULT 12
BQ887729 988 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT 8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
DEFINITION 5', mRNA sequence.

ACCESSION BQ887729
VERSION BQ887729.1
KEYWORDS GI:22279743
SOURCE EST.
ORGANISM Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 988)
AUTHORS NIH-MGC <http://mgc.mci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: Reggen, Invitrogen Corp.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
Plate: LHM13739 row: m column: 06
High quality sequence start: 8
High quality sequence stop: 509.
Location/Qualifiers

FEATURES

source

1..988
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6313133"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_129"
/note="Organ: Olfactory epithelium; Vector: pCMV-SPORT6.1.cdb; Site 1: Score; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.2 kb. Constructed by Reggen, Invitrogen Corp. Note: this is a NIH MGC library."
BASE COUNT 158 a 349 c 300 g 181 t

ORIGIN

Query Match

2.8%; Score 38; DB 13; Length 988;

Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 GACGCTCTTTCGACCTGTCATCGTGCACCTGTG 311
|||||
Db 188 GACGCTCTTTCGACCTGTCATCGTGCACCTGTG 225

FEATURES

source

CA315228 256 bp mRNA linear EST 26-NOV-2002
LOCUS UI-M-FW0-chi-D-15-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
DEFINITION IMAGE: 6809872 5', mRNA sequence.
ACCESSION CA315228
VERSION CA315228.1
KEYWORDS GI:24533352
SOURCE EST.
ORGANISM Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 256)
AUTHORS NIH-MGC <http://mgc.mci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

The following repetitive elements were found in this cDNA sequence: 37-156, >(GGA)nSimple repeat (matched complement) 82-200
>(GAA)nSimple repeat (matched complement) 201-254, >(GGA)nSimple repeat (matched complement)
Seq primer: pTX-5.
Location/Qualifiers

FEATURES

source

1..256
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6"
/db_xref="taxon:10090"
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/tissue_type="whole brain"
/dev_stage="embryo 13.5, 14.5, 16.5, 17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH_BMAP_FW0"
/note="Organ: Brain; Vector: pTX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pTX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP); 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT

7 a 140 c 9 g 100 t

ORIGIN

Query Match 2.7%; Score 36; DB 14; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      892 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 927
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DB      89 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 54
      |||||||

RESULT 14
BG915999      1000 bp      mRNA      linear      EST 05-JUN-2001
LOCUS      602815267F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4937465 5',
DEFINITION      mRNA sequence.
ACCESSION      BG915999
VERSION      BG915999.1 GI:14296475
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 1000)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgabbs-r@mail.nih.gov
      Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
      Ph.D.
      cDNA Library Preparation: Life Technologies, Inc.
      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.llnl.gov
      plate: LLM410871 row: e column: 18
      High quality sequence stop: 486.
FEATURES
      source
      Location/Qualifiers
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             /mol_type="mRNA"
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             /clone="IMAGE:4937465"
             /cissue_type="tumor, gross tissue"
             /dev_stage="5 months"
             /lab_host="DH10B"
             /clone_lib="NCI CGAP Mam4"
             /note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI;
             Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
             Library constructed by Life Technologies. Investigators
             providing samples: Lothar Hennighausen/Priscilla Furth,
             NIH Reference for transgenic model: Li et al., Cell Growth
             and Differentiation 7, 3-11 (1996)."
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BASE COUNT      358 a      202 c      240 g      200 t
ORIGIN
```

```

Query Match      2.7%; Score 36; DB 12; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      892 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 927
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DB      37 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 72
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```

RESULT 15
CA752540/c      578 bp      mRNA      linear      EST 27-NOV-2002
LOCUS      UI-M-FOO-cdo-g-14-0-UI.r1 NIH_BMAP_FOO Mus musculus cDNA clone
DEFINITION      IMAGE: 6831111 5', mRNA sequence.
ACCESSION      CA752540
VERSION      CA752540.1 GI:25583363
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```

REFERENCE      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 578)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgabbs-r@mail.nih.gov
      Tissue Procurement: Dr. Jim Lin, University of Iowa
      cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
      cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
      DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
      Clone Distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.llnl.gov
      This clone was contributed by the Brain Molecular Anatomy Project
      (BMAP)
```

```

The following repetitive elements were found in this cDNA
sequence: 24-142, >(GGA)n#Simple repeat (matched complement)
158-277, >(GGA)n#Simple repeat (matched complement) 301-578,
>RMR17C#LTR_5/6_bp_duplication
Seq primer: pyx-5
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```

FEATURES
      source
      Location/Qualifiers
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             /mol_type="mRNA"
             /strain="C57BL/6"
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             /dev_stage="embryo 12.5dpc"
             /lab_host="DH10B (T1 phage resistant)"
             /clone_lib="NIH BMAP F00"
             /note="Organ: Brain; Vector: pyx-Asc; Site_1: EcoR I;
             Site_2: Not I; The library was constructed according
             Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
             1996. Denatured RNA was size fractionated on a 1% agarose
             gel. First strand cDNA synthesis was primed with oligo-dT
             primer containing a Not I site. Double strand cDNA was
             size selected according to mRNA size fraction, ligated
             with EcoR I adaptor, digested with NotI and then cloned
             directionally into pyx-Asc vector. The library tag
             sequence located between the Not I site and the polyA tail
             is TGAGAGAGCC. This library was created for the University
             Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
             Developing Mouse Nervous System', supported by National
             Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
             program coordinator."
```

```

BASE COUNT      33 a      289 c      24 g      232 t
ORIGIN
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Query Match      2.6%; Score 35; DB 14; Length 578;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      892 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 926
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DB      386 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 352
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Search completed: February 8, 2004, 06:35:51
Job time : 3142.43 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 18:44:02 ; Search time 519.53 Seconds
(without alignments)
10611.687 Million cell updates/sec

Title: US-09-692-077D-1

Perfect score: 1353
Sequence: 1 atggaccacagaccaccta.....ggaccacagcgcgcgcga 1353

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBank :
1: gb_ba :
2: gb_bt :
3: gb_in :
4: gb_om :
5: gb_ov :
6: gb_pac :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_sca :
12: gb_sy :
13: gb_un :
14: gb_vl :
15: em_ba :
16: em_fun :
17: em_hum :
18: em_in :
19: em_mu :
20: em_om :
21: em_or :
22: em_ov :
23: em_pat :
24: em_ph :
25: em_pl :
26: em_ro :
27: em_sca :
28: em_un :
29: em_vl :
30: em_hcg_hum :
31: em_hcg_inv :
32: em_hcg_other :
33: em_hcg_mus :
34: em_hcg_pin :
35: em_hcg_rtd :
36: em_hcg_mam :
37: em_hcg_vrt :
38: em_sy :
39: em_hcgo_hum :
40: em_hcgo_mus :
41: em_hcgo_other :

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353	100.0	1353	6	AX350489 Sequence
2	1353	100.0	9842	6	AF005900 Homo sapi
3	1349.8	99.8	2072	6	AR270618 Sequence
4	1349.8	99.8	2072	6	AR270618 Sequence
5	1349.8	99.8	2072	6	AR270618 Sequence
6	1325	97.9	1344	6	AX350490 Sequence
7	1325	97.9	1344	6	AX350490 Sequence
8	1321.8	97.7	22842	9	AC092603 Homo sapi
9	1159.2	85.7	1356	4	AY150333 Homo sapi
10	1046	77.3	1987	10	CPU25723
11	989.2	73.1	1639	10	RNA2BRRA
12	988.8	73.1	6268	10	AF366899
13	988.8	73.1	124474	2	AC126878
14	984	72.7	22319	10	RA22BR
15	977.8	72.3	276543	2	AC112830
16	977.6	72.3	1347	10	AF332049
17	977.6	72.3	1650	10	MUSADRENH
18	976	72.1	1347	10	AF332050
19	976	72.1	83802	10	AL731836
20	975.2	72.1	1185	10	ASP427259
21	968	71.5	1185	10	ED0427270
22	967.4	71.5	1180	9	NC0521186
23	965.4	71.4	1171	9	CVA251182
24	964.6	71.3	1203	4	TRE315939
25	962.6	71.1	1191	10	CCA427260
26	961	71.0	1168	4	TR251187
27	960.6	71.0	1197	4	LCR427254
28	960	71.0	9377	10	MUSADRENCA
29	957.4	70.8	1183	4	OCAR2B
30	954.6	70.6	1197	4	LP315941
31	951.8	70.3	1185	10	GGL427258
32	950	70.2	1198	4	ECAR2B
33	949.4	70.2	1183	4	OCY16189
34	948.8	70.1	1180	4	LP505821
35	945.4	69.9	1177	4	BPR251175
36	939.8	69.5	1180	4	HAM251178
37	938.4	69.4	1186	4	MSP251185
38	938.2	69.3	1172	10	ARU427256
39	937.6	69.3	1179	10	TPA427266
40	936.2	69.2	1197	4	MTE505820
41	932.4	68.9	1162	4	FCA251174
42	932.2	68.9	1185	4	AF337541
43	931.4	68.8	1174	4	PCA427417
44	931.2	68.8	1168	4	PVI251176
45	930	68.7	1176	4	LAL315940

ALIGNMENTS

RESULT 1
LOCUS AX350489 1353 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 1 from Patent WO0179561.
ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 1 25-OCT-2001;

Pred. No. is the number of results predicted by chance to have a

FEATURES
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 Location/Qualifiers
 1.1353
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
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 BASE COUNT 224 a 458 c 405 g 266 t
 ORIGIN

Query Match 100.0%; Score 1353; DB 6; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 8.9e-218;
 Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGACACAGAGACCCCTACTCCGTCAGAGCCAGAGGCGCCATGCGGCGCCATCAC 60
 Db 1 ATGAGACACAGAGACCCCTACTCCGTCAGAGCCAGAGGCGCCATGCGGCGCCATCAC 60
 QY 61 TTCTCATCTCTTTTACATCTTTCGAGCAAGCTGTGATCTCTGCTGTGTGACAGC 120
 Db 61 TTCTCATCTCTTTTACATCTTTCGAGCAAGCTGTGATCTCTGCTGTGTGACAGC 120
 QY 121 CGCTGCTGCGCGCCCTCAGAACCTGTTCTGCTGTGTGCTGCGCGCCGCGCATCTCTG 180
 Db 121 CGCTGCTGCGCGCCCTCAGAACCTGTTCTGCTGTGTGCTGCGCGCCGCGCATCTCTG 180
 QY 181 GTGGCAGGCTCATATCTCTTCTGCTGCGCAAGAGCTGTGAGCTACTGTAATTC 240
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 Db 301 GTGACCTGTGCGCCATCAGCTGAGACCGTACTAGGCGCGGAGCGCGCTGAGATAC 360
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 Db 361 AACTCCAAAGGCGACCCCGCGCGCATCAAGTGCATCTCTCACTGTGTGCTCATCGCC 420
 QY 421 GCCGTCATCTGCTGCGCGCCCTCATCTAACAAGGCGACAGAGGCGCGCGCGCGG 480
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 Db 841 GGCAGAGGCGCAGAGAGAGGTGTTGTGGGCGATCTCCAGAGAGATGAAGCTGAAGAGAG 900

QY 901 GAAG 960
 Db 901 GAAG 960
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 QY 1261 CTGAACCTGTTATCTTACACATCTTCAACAGAGACTTCCGCGTCCGAGAGATC 1320
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 QY 1321 CTGTGCGCGCGGTGAGACCAAGCGGCGTGGGA 1353
 Db 1321 CTGTGCGCGCGGTGAGACCAAGCGGCGTGGGA 1353

RESULT 2
 AF005900 9842 bp DNA linear PRI 08-JUL-1997
 AF005900
 LOCUS Homo sapiens alpha2B-adrenergic receptor (alpha2C2AR) gene.
 DEFINITION complete cds.
 ACCESSION AF005900
 VERSION AF005900.1 GI:2245627
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 9842)
 Cayla,C., Schack,S., Bouloumie,A., Davedjian,J.C. and Paris,H.
 Alpha2C2-adrenergic receptor gene
 JOURNAL Unpublished
 2 (bases 1 to 9842)
 Cayla,C., Schack,S., Bouloumie,A., Davedjian,J.C. and Paris,H.
 Direct Submission
 JOURNAL Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,
 CHU Rangueil, Toulouse 31403, France
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
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 5398..6750
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 /note="adrenergic receptor"
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 /product="alpha2B-adrenergic receptor"
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gene
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BASE COUNT	1870 a	2747 c	3225 g	1998 t
ORIGIN				2 others

Query Match	100.0%;	Score 1353;	DB 9;	Length 9842;
Best Local Similarity	100.0%;	Pred. No. 7e-218;		
Matches 1353;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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VLATRGVLLIGRVSAGIIGDOMMRRAOALTREKREIVAVIYAVYGCALPFFPFSYS
LGATICPKHKCKVPHLPGFPFWMTCYNSLSNPVLYITIPNDQPRABRPRILICRPMQTAM

OY	1	TTGAGCAACAGAGAACCCCTACCTCGGTGAGAGCAACAGAGGGGCAATGAGCGGCGCCATCAAC	60
Db	5398	ATTGAGCAACAGAGAACCCCTACTTCGTTGACAGGCACACAGGCGCCATTAAGCGGCGCCATCAAC	5455
OY	61	TTTCTCATTTCTTTACCATCTTTGCGGCAACGCTCTGTATCATCTGGCTGTGTGAACAGC	120
Db	5458	TTTCTCATTTCTTTACCATCTTTGCGGCAACGCTCTGTATCATCTGGCTGTGTGAACAGC	5511
OY	121	CGCTTCGTGCGCGCCCTCAGAACCTGTTCCTGTGTGCTGTGGCCGCGCGGCAATCCTG	180
Db	5518	CGCTTCGTGCGCGCCCTCAGAACCTGTTCCTGTGTGCTGTGGCCGCGCGGCAATCCTG	5572
OY	181	GTGGCCAGGCTCATATCCCTTTTCGCTGGGCAACAGACGTCTGAGGCTACCTGATCACTTC	240
Db	5578	GTGGCCAGGCTCATATCCCTTTTCGCTGGGCAACAGACGTCTGAGGCTACCTGATCACTTC	5633
OY	241	CGGCGACAGTGTGCGAGGTGTACTGTGGCGCTCGACGTGTCTTTCTGACCTGTATCATC	300
Db	5638	CGGCGACAGTGTGCGAGGTGTACTGTGGCGCTCGACGTGTCTTTCTGACCTGTATCATC	5697
OY	301	GTGCACCTGTGTGCGCATCAGCTTGACCGGCTACTGGGCGGTGAGCGCGGCGCTGGAATAC	360
Db	5698	GTGCACCTGTGTGCGCATCAGCTTGACCGGCTACTGGGCGGTGAGCGCGGCGCTGGAATAC	5757
OY	361	AACTCCAAAGCGCAACCCGCGCGCGGATCAAGATCATATCTCACTGTGTGCTCATCGCC	420
Db	5758	AACTCCAAAGCGCAACCCGCGCGCGGATCAAGATCATATCTCACTGTGTGCTCATCGCC	5817
OY	421	GCCGTCAATCTCGCTGCGCGCCCTCATCTTACAAGGGCGACCAAGGGCCCCAGCGCGCGAG	480
Db	5818	GCCGTCAATCTCGCTGCGCGCCCTCATCTTACAAGGGCGACCAAGGGCCCCAGCGCGCGAG	5877
OY	481	CGCCCCAGTGCAGCTTCAACGAGAGGCTGTATCATCTGTGGCTTCCAGCATCGGATCT	540
Db	5878	CGCCCCAGTGCAGCTTCAACGAGAGGCTGTATCATCTGTGGCTTCCAGCATCGGATCT	5937
OY	541	TTCTTTGCTCCTTGGCTCATATCATATATCTGTCTATCGGCGATCTACCTGATCGCCAAA	600
Db	5938	TTCTTTGCTCCTTGGCTCATATCATATATCTGTCTATCGGCGATCTACCTGATCGCCAAA	5997
OY	601	CGACGCAACCGCAGAGGTCCACGAGGCCAAGAGGGGGGCTGTGGCAGAGGTGATCCAGACG	660
Db	5998	CGACGCAACCGCAGAGGTCCACGAGGCCAAGAGGGGGGCTGTGGCAGAGGTGATCCAGACG	6055
OY	661	CCCGACCCGACCATGTGTGGGCTTTGGCTTCAAGCAATGACAGCCCTGTGGCTTGTG	720
Db	6058	CCCGACCCGACCATGTGTGGGCTTTGGGCTTCAAGCAATGACAGCCCTGTGGCTTGTG	6117
OY	721	GCTTTCGACAGAGAGTCAACGGAACCTCGAATCTCACTGGGGGAATAAGAGAGGGGGAG	780
Db	6118	GCTTTCGACAGAGAGTCAACGGAACCTCGAATCTCACTGGGGGAATAAGAGAGGGGGAG	6177
OY	781	ACCCCTGAAGATCTGTGGACCCGGGCGCTTGACACCAAGTTGGGCTGCCCTTCCAACTCA	840
Db	6178	ACCCCTGAAGATCTGTGGACCCGGGCGCTTGACACCAAGTTGGGCTGCCCTTCCAACTCA	6233
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[illegible]

RESULT 3					
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LOCUS	AR270618	2072 bp	DNA	linear	PAT 10-APR-2003
DEFINITION	Sequence 1181 from patent US 6500938.				
ACCESSION	AR270618				
VERSION	AR270618..1	GI:29701852			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2072)				
TITLE	Au-Young J. and Seilhamer J.J.				
JOURNAL	Composition for the detection of signaling pathway gene expression				
FEATURES	Patent: US 6500938-A 1181 31-DEC-2002;				
	location/Qualifiers				

source	1..2072	/organism="unknown"
BASE COUNT	316 a 705 c 660 g 391 t	
ORIGIN		
Query Match	99.8%	Score 1349.8; DB 6; Length 2072;
Best Local Similarity	99.9%	Pred. No.2.9e-217;
Matches 1351; Conservative	0; Mismatches 2;	Indels 0; Gaps 0;

Oy	1	ATGAGCACCAAGAGACCCCTACTCGGTGACGGCCACAGCGGCAATAGCGGCGGCATCAAC	60
Db	413	ATGAGCACCAAGAGACCCCTACTCGGTGACGGCCACAGCGGCAATAGCGGCGGCATCAAC	472
Oy	61	TTCCCTCAATTCCTTTAACCATCTTGGGACAGCTCTGGTCAATCGTGCTGTGTGTAACCAAC	120
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Db	533	CGCTCGGCGGCGGCGCCCTCAGAACTGTCTCTGGTGTGCTGGCGCGCGCGCGCATCTCGT	592
Oy	181	GTGGCCACGCTCAATCAATCCCTTTCTCGGTGGCCACGAGCTGCTGGGCTACTGTGTAATTC	240

Db	593	GTGGCAACGCTATCATTCCTTTCTTCGCTGGCCAAAGAGCTGTGGGCTACTGTACTTC	652
QY	241	CGGCGCAAGTGTGCGAGGTGTAACTGGCGCTCGACGCTCTTCTGCACTCGTGCATC	300
Db	653	CGGCGCAAGTGTGCGAGGTGTAACTGGCGCTCGACGCTCTTCTGCACTCGTGCATC	712
QY	301	GTGCACTGTGGCCATCAGCTGTGAACGGCTAATGGGCGGTGACCGCGGCTGTAGTAC	360
Db	713	GTGCACTGTGGCCATCAGCTGTGAACGGCTAATGGGCGGTGACCGCGGCTGTAGTAC	772
QY	361	AACCTCAAGCGCAACCCGCGCGCATCAAGTCATTCCTCACTGTGTGGCTCATCGCC	420
Db	773	AACCTCAAGCGCAACCCGCGCGCATCAAGTCATTCCTCACTGTGTGGCTCATCGCC	832
QY	421	GCCGCTCATCTGGCTGCGCGCCCTCATCTCAAGGCGCAACAGGCCCCAGCCGCGG	480
Db	833	GCCGCTCATCTGGCTGCGCGCCCTCATCTCAAGGCGCAACAGGCCCCAGCCGCGG	892
QY	481	CGCCCCAGTGCAAAGCTTCAACAGAGAGCGTGTATCATCTGTGCTTCAGACATCGAAT	540
Db	893	CGCCCCAGTGCAAAGCTTCAACAGAGAGCGTGTATCATCTGTGCTTCAGACATCGAAT	952
QY	541	TTCTTTGTCTCTTCCCTCATCAGATTCCTTGTCTAAGCTGGCATCTAAGTCGCAAA	600
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Db	1073	CCCCGACCGACCATGGTGGGGGCTTTGGCTCAGCCAACTGCCAGCCTGGCTCTGTG	1132
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Db	1133	GCTTCTTGCCAGAGAGTCAACGCACTCGAAGTCACTGGGGAAGAAAGAGAGGGAG	1192
QY	781	ACCCCTGAAGATATCTGGGACCCGGGCTTGGCCAACCAAGTTGGGCTGCCCTTCCAACTCA	840
Db	1193	ACCCCTGAAGATATCTGGGACCCGGGCTTGGCCAACCAAGTTGGGCTGCCCTTCCAACTCA	1252
QY	841	GCGCAGGGCCAGAGAGAGGTGTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG	900
Db	1253	GCGCAGGGCCAGAGAGAGGTGTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG	1312
QY	901	GAAAGGAGAGAGAGAGAGAGAAAGTGTGAACCCAGGCAAGTGCAGATGTCTCCGGCC	960
Db	1313	GAAAGGAGAGAGAGAGAGAGAAAGTGTGAACCCAGGCAAGTGCAGATGTCTCCGGCC	1372
QY	961	TCAGCTTGGACGCCCCGCTGCAGAGCAACAGGAGCTCCGGGGCTGGGCAACCTTACGT	1020
Db	1373	TCAGCTTGGACGCCCCGCTGCAGAGCAACAGGAGCTCCGGGGCTGGGCAACCTTACGT	1432
QY	1021	GCGCAGGTGCTCTTGGGCAAGGGGCGTGGGTGTAAAGTGTGGCAGTGTGGCTGCAAG	1080
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QY	1141	GTGCTCTGCTGTTCCCTTTCTTTCAGCTAACAGCTTGGGCGCATCTGGCCGAAGCAC	1200
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QY	1201	TGCAAGGTGCCCATGTGCGCTCTTCAAGTCTTCTCTCGATGTGGCTACTGTCAACAGCTCA	1260
Db	1613	TGCAAGGTGCCCATGTGCGCTCTTCAAGTCTTCTCTCGATGTGGCTACTGTCAACAGCTCA	1672
QY	1261	CTGAACCTCTGTATCTACACCATCTTCAACACAGACCTTCGCGCGTGTCTTCGGAGGATC	1320
Db	1673	CTGAACCTCTGTATCTACACCATCTTCAACACAGACCTTCGCGCGTGTCTTCGGAGGATC	1732

QY	1321	CTGTGCGCCGGTGGAGACCAGACGGCTGTGTGA	1353
Db	1733	CTGTGCGCCGGTGGAGACCAGACGGCTGTGTGA	1765
<hr/>			
RESULT 4			
HUMADRA2R			
LOCUS	HUMADRA2R	2072 bp	DNA linear PRI 30-OCT-1998
DEFINITION	Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.		
ACCESSION	M34041		
VERSION	M34041.1	GI:178197	
KEYWORDS	alpha-2-adrenergic receptor; plasma membrane protein;		
SOURCE	receptor-coupled G protein.		
ORGANISM	Homo sapiens (human)		
	Bukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 2072)		
AUTHORS	Lomasney,J.W., Lorenz,W., Allen,L.F., King,K., Regan,J.W., Yang-Peng,T.L., Caron,M.G. and Lefkowitz,R.J.		
TITLE	Expansion of the alpha 2-adrenergic receptor family: cloning and characterization of a human alpha 2-adrenergic receptor subtype, the gene for which is located on chromosome 2		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)		
MEDLINE	90311349		
PUBMED	2164221		
COMMENT	Original source text: Human placenta DNA, clone alpha-2 C2. Draft entry and computer-readable sequence for (1) kindly submitted by J.W.Lomasney, 03-MAY-1990, for release after publication.		
FEATURES	Location/Qualifiers		
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BASE COUNT	316 a	705 c	660 g
ORIGIN	Chromosome 2.		
Query Match	99.8%;	Score 1349.8;	DB 9;
Best Local Similarity	99.9%;	Pred. No. 2.9e-217;	Length 2072;
Matches 151;	Conservative 0;	Mismatches 2;	Indels 0;
	Gaps 0;		
QY	1	ATGACCAACAGAGACCCCTACTCGTCGACAGCACAGCGGCATTAGCGGCATTACAC	60
Db	413	ATGACCAACAGAGACCCCTACTCGTCGACAGCACAGCGGCATTAGCGGCATTACAC	472
QY	61	TTTCGATTGCTTTTACCATCTTCGGCAAGCTCTGCTGATCCTCGCTGTGTTGACCAAC	120
Db	473	TTTCGATTGCTTTTACCATCTTCGGCAAGCTCTGCTGATCCTCGCTGTGTTGACCAAC	532
QY	121	CAGTCGCTGCGGCCCTCAGAAGCTGTTCTGAGTAGTCGCTGAGCGCGCGGACGACATCCG	180
Db	533	CAGTCGCTGCGGCCCTCAGAAGCTGTTCTGAGTAGTCGCTGAGCGCGCGGACGACATCCG	500

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361 AACTCCAAAGCAGCAGCCCGGCGGCATCAAGTGCATCATCTCACTGTGTGCTCATCGCC 420
773 AACTCCAAAGCAGCAGCCCGGCGGCATCAAGTGCATCATCTCACTGTGTGCTCATCGCC 832
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833 GCGGTATCTGCTGCTGCGCCCTCATCTACAAAGGAGCAGGAGCGCCGCGCGG 892
481 CCGCCCATGTGCAAGCTCAACCGAGGCTGTGTAATCTGTGCTTCAGCATCGGATCT 540
893 CCGCCCATGTGCAAGCTCAACCGAGGCTGTGTAATCTGTGCTTCAGCATCGGATCT 952
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661 CCGCCCATGTGCAAGCTCAACCGAGGCTGTGTAATCTGTGCTTCAGCATCGGATCT 720
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781 ACCCTGGAAGATACCTGGGACCCGAGGCTTGGCCAGCAGTGTGGCTGCTCCCACTCA 840
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LOCUS AX548756 3274 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 41 from Patent WO02061087.
ACCESSION AX548756
VERSION AX548756.1 GI:25813686
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Burnier, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 41 08-AUG-2002;
LifeSpan Biosciences, Inc. (US)
Location/Qualifiers

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BASE COUNT 587 a 979 c 967 g 741 t
ORIGIN

Query Match 99.8%; Score 1349.8; DB 6; Length 3274;
Best Local Similarity 99.9%; Pred. No. 2.8e-217;
Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS Sequence 2 from Patent WO0179561.
ACCESSION AX350490
VERSION AX350490.1 GI:18616092
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms

JOURNAL Patent: WO 0179561-A 2 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
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Query Match 97.9%; Score 1325; DB 6; Length 1344;
Best Local Similarity 99.3%; Pred. No. 4,6e-213;
Matches 1344; Conservative 0; Mismatches 0; Indels 9; Gaps 1;
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REFERENCE AUTHORS TITLE JOURNAL	4 (bases 1 to 22842) Waterston,R.H. Direct Submission Submitted (20-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE AUTHORS TITLE JOURNAL	5 (bases 1 to 22842) Waterston,R.H. Direct Submission Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE AUTHORS TITLE JOURNAL	6 (bases 1 to 22842) Waterston,R. Direct Submission Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Oct 20, 2001 this sequence version replaced ga114916188.
COMMENT	

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPEC-11 human BAC library was made from the blood of one male donor, as described by Oogesawa, K., Moon, P.-Y., Zhao, B., Frengen, B., Tatemoto, M., Cattanese, J.J., and de Jong, P.J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.researchgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
PIECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
the clone sequenced to the right is RP11-574O17, 2000 bp overlap.
The clone sequenced to the right is RP11-574O17, 2000 bp overlap.
Actual end of this clone is at base position 48999 of RP11-574O17.
Polymorphisms have been identified between AC013272 and AC092603.

The sequence of AC073396 has been incorporated into AC092603.

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DEFINITION Tupaiia belangeri alpha-2B adrenoceptor mRNA, complete cds.
VERSION AY150333
KEYWORDS
SOURCE
ORGANISM
Tupaiia belangeri (tree shrew)
Tupaiia belangeri
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Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
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Helbronner, U., van Kampen, M., Isovich, E. and Fluegge, G.
Thalamic alpha-2B adrenoceptors under chronic stress: persistent
upregulation in the paraventricular nucleus
Unpublished
2 (bases 1 to 1356)
Fluegge, G. and Meyer, H.
Direct Submission
Submitted (13-SEP-2002) Neurobiology, German Primate Center (DPZ),
Kellnerweg 4, Goettingen 37077, Germany
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VERSION      U25723.1 GI:818876
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REFERENCE
AUTHORS      Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and
                Regan,J.W.
TITLE      Heterologous expression of the cloned guinea pig alpha 2A, alpha
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JOURNAL      Biochem. Pharmacol. 51 (3), 291-300 (1996)
MEDLINE      96152573
PUBMED      8573196
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PUBMED      2 (bases 1 to 1987)
AUTHORS      Richman,J.G.
TITLE      Direct Substitution
JOURNAL      Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
                Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
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Qy      241 CGGCGCGAGGTGTGAGAGGTATACCTGTGAGAGTGTCTTCTGACACTTCCTGCAATC 300
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Qy      301 GTGCACTGTGAGGCAATGAGCTGAGACGCTACTGAGGCGCGCGCGCGCGCGCGCGCG 360
Db      628 GTGCACTGTGAGGCAATGAGCTGAGATGCTACTGAGGCGCGCGCGCGCGCGCGCGCG 687
Qy      361 AACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db      688 AACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 747
Qy      421 GCGGTATCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db      748 GCGGTATCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 805
Qy      481 CGCGCCAGTGAAGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db      806 -GTCCCAATGGAAGTGAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 864
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Db      865 TTCTTGTGACCTTGTCTCATATGATCTGTGTACTGTGCGATTTAACTGATGCGCAAG 924
Qy      601 CGCAGCAACCGAGAGTCCAGAGGCGCAAGGAGGAGGCTGGCGAGAGTGAAGCAG 660
Db      925 CGCAGCAACCGAGAGGAGTCCAGAGGCGCAAGGCGGCGCGAGGAGGAGTCAAGGAG 984
Qy      661 CCCCGAACCGACATGTGGGCTTTGGCTCAAGCCAACTGCGAGCTTGGCT---CT 717
Db      985 TCTGTCTTGAAGCCCGAGAGGAGCTCAAGCTTGTGCAAGGTGCAACCTTGGCTTCACT 1044
Qy      718 GTGGCTTTCAGAGAGGTCAACGAGCACTGGAAGTCACTGGGAGAGAGAGAGAGAG 777

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OY 421 GCCGTCATCTCGTCGCGCCGCTCATCTTACAGAGGCGACCGGCGCCGCGCGG 480
Db 3215 GCGTGTATTTCTTACCGCCCTCATCTTACAGAGGCGACCGGCGCCGCGCGG 3274
OY 481 CCGCCCAAGTGAAGCTCAACCAAGAGGCTGTATCTGTGCTTCAGCATCGATCT 540
Db 3275 CTCCCCAGTGTAGCTCAACCAAGAGGCTGTATCTGTGCTTCAGCATCGATCT 3334
OY 541 TTTCTTGTCTCTGCTCATCATGATCTGTCTTACCTGGGCTTACCTGATCGCAMA 600
Db 3335 TTTTGTCTCTGCTCTCATCATGATCTGTCTTACCTGGGCTTACCTGATCGCAMA 3394
OY 601 CCGAGCAACCGCAAGAGTCCCAAGGCGCCAGGCGGCGCTGCGAGGAGTCAAGCAG 660
Db 3395 CCGAGCAACCGCAAGAGTCTCGAGGCGCAAGAGGCGCTGCGAGAGGAGTCAAGAG 3454
OY 661 CCCCAGCCGACCATGTGTGGGCTTTGGCTTCAGCCAACTGCCAGCCTTGCTGCT 717
Db 3455 CCCCAGCCGCTTGTCTGGGAGTGGCAACCTCAGCTTAAAGTGGCCCACTCTGCT 3514
OY 718 GTGGCTTCTCCAGAGAGTCAACGCACTCGAAGTCCAGTGGGAGAGAGAGAGG 777
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OY 958 GCCTCAGCTTGCAGCCCGCTGTCAGCAGCAGGCGCTCCCGGCTGTCGACCATTA 1017
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OY 1018 CGTGGCCAGGTGCTCTCTGCGCAGGCGCTGCTGCTATAGTGTGGCAGTGTGCT 1077
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OY 1258 TCACAGAACCTGTATCTACACATCTTCAACAGAGACTTCCGCGTGTCCGAG 1317
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OY 1318 ATCTGTGCGCGCGCTGAGACCAAGAGCGCTGTGA 1353
Db 4106 ATCTGTGCGCGCGCTGAGACCAAGAGCGCTGTGA 4141

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RESULT 13
AC126878 124474 bp DNA linear HTG 15-NOV-2002
LOCUS Ratius norvegicus clone CH230-263M16, WORKING DRAFT SEQUENCE, 2
DEFINITION
unorderd pieces.
ACCESSION
AC126878
VERSION
AC126878.4 GI:25007910
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

```

SOURCE	ORGANISM	REFERENCE	AUTHORS
Rattus norvegicus (Norway rat)	Rattus norvegicus	1 (bases 1 to 124474)	Allen, J., Marle, Metzer, M. Lee, Abramson, S., Adams, C., Alder, J., Muzny, D., Marle, Metzer, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amn, A., Angilano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bunay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Diaper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Gervais, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hui, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lohnsuhewa, L., Louiseged, H., Lozado, R. J., Lu, X., Ma, D., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, B., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nait, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankweli, O., Okunolu, G., Olarnunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankuch, C., Plopper, F., Polindexter, A., Popovic, D., Prims, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Register, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sherty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smaj, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrell, R., Soza, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uman, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yeon, L., Yeon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.
Rattus norvegicus	Rattus norvegicus	2 (bases 1 to 124474)	Worley, K. C.
Rattus norvegicus	Rattus norvegicus	Submitted (10-JUL-2002)	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Rattus norvegicus	Rattus norvegicus	3 (bases 1 to 124474)	Human Genome Sequencing Consortium.

On Nov 15, 2002 this sequence version replaced gi:23907627. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing results (rat/). Each contig described (<http://www.hgsc.bcm.tmc.edu/projects/rat/>).

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Db	58635	TTCTGTGCTGCTGCGGTCTCTTCTCTTTTCAGCTACAGCTGGGGGCACATCGCCACAG	58694
Qy	1198	CATCGCAAGGTGCCCATGAGCTCTTTCAGTCTCTTCTTGATTCGGCTACTGCAACAGC	1257
Db	58695	CATCGCAAGGTACCGGACATGGGCTCTTTCAGTCTCTTCTTGATTCGGCTACTGCAACAGC	58754
Qy	1258	TCACCTGAACCTGTATATCTACACCATTTTCAACCAAGGACTTCCGCCGTGCTTCCGGAAG	1317
Db	58755	TCCTTGAACCTGTATATCTACACCGCTTTCACACCAAGGACTTCCGCCGTGCTTTCGAAG	58814
Qy	1318	ATCTGTGCGCGCCGCTGAGACCCAGAGCGCCGTGGA	1353
Db	58815	ATCTGTGCGCGCCGCTGAGACCCAGACTGGCTGGTGA	58850

RESULT 14			
LOCUS	RAT2ABR	2319 bp	mRNA
DEFINITION	Rat alpha-2B-adrenergic receptor		linear
ACCESSION	M32061		ROD 27-APR-1993
VERSION	M32061.1	GI:202589	
KEYWORDS	adrenergic receptor.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBLISHED	COMMENT
1 (bases 1 to 2319)	Zeng,D.W., Harrison,J.K., D'Angelo,D.D., Barber,C.M., Tucker,A.L., Lu,Z.H. and Lynch,K.R.	Molecular characterization of a rat alpha 2b-adrenergic receptor	Proc. Natl. Acad. Sci. U.S.A.	87 (8), 3102-3106 (1990)	
				90222177	
				2158103	
					Original source text: Rat (strain Sprague Dawley) adult kidney,

FEATURES

Draft entry and computer-readable sequence [1] kindly submitted by K.R. Lynch, 12-FEB-1990.

Location/Qualifiers

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source
1. .2319
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/sex="male"
/tissue_type="kidney"
/dev_stage="adult"
1. .2319
gene
/gene="RNG-alpha-2"
366. .1727
CDS

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BASE COUNT	433 a	700 c	618 g	568 t
ORIGIN				
Query Match		72.7%;	Score 984;	DB 10; Length 2319;

Best Local Similarity 84.0%; Pred. No. 9.4e-156;
Matches 1139; Conservative 0; Mismatches 205; Indels 12; Gaps 2;

OY	1	ATGACACACAGAGACCCCTTACTCCGTGACAGGCCACAGCGGCACATAGGAGGGGACCATACG	60
Db	381	ATGACACCATAGAGAGCCCTACTCGTGTACAGGCCACGCGGCACATCGGTGGCCATACG	440
OY	61	TTCCATCTTCTTTTACCATCTTTCGAGCAAGCTCTGGTCAATCCGTGCTGTGTACCGAGC	120
Db	441	TTTCTCATCTCTTTTACCATTTTTCGGAATGCGCTGGTCAATTGCTGTGTGTACCGAGC	500
OY	121	CGCTCGCTGCGCGCCCTCAGAACTGTCTGTGTGTGCTGGCCGCGCGACATCTCTG	180
Db	501	CGCTCATCCGTGACACCAAAAACGTGTTCTGTGTGTCACTGGACAGACGCCAATCTTA	560
OY	181	GTGGCCACGCTCATATCCCTTTCTCGCTGGGCCCAAGAGCGTGGGCTACTGGTACTCTC	240
Db	561	GTGGCTACTCTCATCATCTCCCTTCTCTCTGTGACCAAGACTGGCTGGGCTACTGGTACTTC	620
OY	241	CGGGGCACTGTGTGTCAGAGTGTACTTGGCCCTCGACGTGTCTTCTGCACTCTGTCAATC	300
Db	621	TGGGTGTGTGTGTGTGTCAGAGTGTACTTGGCCCTAGAGGTGCTTCTGTACTCTCTCATC	680
OY	301	GTGCACTGTGTGCGCATCAAGCTGTGAAACGCTACTTGGGCCGTGAGCCGCGCTGTGAGTAC	360
Db	681	GTGCACTGTGTGTGCATCACTACCTGTGAAAGGTACTGGGCACTGTGAACTTGGAATAC	740
OY	361	AACCTCAAAAGGCAACCCGGGCGCGCATGAGTGATCATATCCCACTGTGTGCTCATGACC	420
Db	741	AACCTCAAGGCACTCCGTGTCCGCATGAGTGATCATCTCTCACTGTGTGTCTAATTGTGCA	800
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Db	801	GCCTCATTTTCTTCTACCGGCCCTCATCTACAAGGGACCAAGCGCCGACGCGCGGG	860
OY	481	CGCCCCAGTGTGCAAGCTTCAACCAAGAGGCGCTGTGTACATCTGTGGCTTCAAGATGTGATCT	540
Db	861	CTCCCCAGTGTGTGCTTCAACCAAGAGGCGCTGTGTACATCTTGTGGCTTCAAGATGTGATCT	920
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OY	661	CCCCGACCCGACATGTGTGGGGCTTTTGGCTCTAGCCAAATCTGCCAGCCCTTGGCT---	717
Db	1041	CCCCAGCGGTGTGTGGGGAGTGTCCAACTCAAGCTTAAAGTGGCCACCTGTGTCTTCTCT	1100
OY	718	GTGGCTTCTGTCACAGAGGTCAACGAGCACTCGAAGTCTCACTGGGAGAAAGAGAGAGGG	777
Db	1101	CTTATCTTCTGTGTGAGAGGCCAATGTGACACCCCAAGCTCTCAAGAGAAAGAGAGAGGG	1166
OY	778	GAGACCCCTGAAGATCTGGGACCCGGGCGCTTGTGCACCCAGTGGGCTGCCCTTCCCAAC	837
Db	1161	GAGACCCCTGAAGATCTGAAGGCCAGGGGCTTTTGGCCCCCACTTGTGTGCTTCCGAGA	1220
OY	838	TCAGGCCAGGGCCAGAAAGAGAGGTGTTTTGTGGGCAATCTCCAGAGATGTAAAGCTGAAAG	897
Db	1221	TCAGGCCAAGGCCAGAAAGAGAGGAGCTTATGTGTGGCGACTGTGAGAGAGAGGAGATGAAG	1280
OY	898	GAGAGAGAGAGAGAGAGAGAGAGAGAGTGTAAACCCCAAGGAGTGTGCCAGTGTCTCCG	957
Db	1281	GATGA-----GGAAGAGTGTGAAGATGTAAACCCCAACCACTGTGCCAGATCTTCT	1331
OY	958	GCTTCAAGTTGTCAAGCCCCCGGCTGACAGCCAGCGGCTCCGGGTGTGTGCAACCTTA	1017
Db	1332	GCTTCAAGTTGTCAAGCCCCCTTGCACAGGCTCAGACTTCTCGGGTATCTGTGGCAACTT	1391
OY	1018	GTGGCCAGGTGTCTTGTGGGAGGGGCTGGGTCTATAGTGTGGGCAAGTGTGTGCGTGA	1077

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Db      1392 CGTGGCAGAGTCTCTTCTGCGGAGAAATGCGAGTTCAGATGCGCAGATGCGCAGAG 1451
QY      1078 AGGGGCGAGCTGACCCGGGAGAGCGCTTACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
Db      1452 CGGACACAGCTGAGCCGGGAGAAAGAGTTCACCTTTGTGTGCGCGTGGCATTTGAGAT 1511
QY      1138 TTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
Db      1512 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1571
QY      1198 CACTGCAAGTGGTCCCATGAGCTCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
Db      1572 CACTGCAAGTGGTCCCATGAGCTCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1631
QY      1258 TCACGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
Db      1632 TCTTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1691
QY      1318 ATCTGTGCGCGCGCGCTGAGACCCAGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1353
Db      1692 ATCTGTGCGCGCGCGCTGAGACCCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1727

RESULT 15
AC112830
LOCUS      276543 bp DNA linear HTG 21-SEP-2002
DEFINITION Rattus norvegicus clone CH230-46115, *** SEQUENCING IN PROGRESS
ACCESSION AC112830
VERSION   GI:21266028
KEYWORDS  HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
           Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
REFERENCE 1 (bases 1 to 276543)
AUTHORS   Muzny, D., Marle, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
           Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
           Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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           Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
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           Egan, A., Ebecro, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
           Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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           Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, C.,
           Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
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           Hollins, B., Howells, S., Hu, Y., Hume, J., Idelbird, D., Jackson, A.,
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Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sander, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvarcberg, A., Sisson, I., Sitter, C.D., Smaj, D.,
Sneed, A., Sodergren, F., Song, X.-Z., Sorrell, R., Soza, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usman, K.,
Vales, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Williams, R., Wleczek, R., Woodson, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, D., Zhou, J., Zhou, X., Zhao, S., Zhou, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G., and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 276543)
Worley, K.C.
Direct Submission
Submitted (25-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 276543)
Baylor Genome Sequencing Consortium.
Direct Submission
Submitted (21-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 21, 2002 this sequence version replaced gi:21743229.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.bgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.bgsc.bcm.tmc.edu/
Contact: bgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GRPO
Center clone name: CH230-46115
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 237012 bases at least Q40
Consensus quality: 239346 bases at least Q30
Consensus quality: 240985 bases at least Q20
Estimated insert size: 252028; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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NOTE: Estimated insert size may differ from sequence length
(see http://www.bgsc.bcm.tmc.edu/docs/Genbank_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1
275384: contig of 275384 bp in length
275385
275485
276543: contig of 1059 bp in length.
Location/Qualifiers
1. 276543
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ORIGIN
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Query Match 72.3% Score 977.8; DB 2; Length 276543;
Best Local Similarity 84.2%; Pred. No. 5.7e-155;
Matches 1142; Conservative 0; Mismatches 202; Indels 13; Gaps 3;

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DB 109602 TTCTCATCTCTTTCACCATTTTGGCAATGCGCTGTGATCTCTGCTGTGTGGTACAGC 109661
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DB 110022 CTCCCGAGTGTGTCAACAGAGGCGTGTGATCTGTGCGCTGTCAAGATCGATCT 110081
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DB 110082 TTTTGTGCTCTGTCTCATCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 110141
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DB 110202 CCCCGACCGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 110261
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QY 718 GTGCTTCTGTGCGAGAGGTGTCAACGCACTGCAAGTGTCACTGTGGGAGAGAGAGAGG 777
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DB 110382 TCAGGCCAGGCGCAGAGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 110441
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QY 1018 CGTGGCAGAGTGTCTCTGTGGCAGGCGCGTGGGTGTATAGGTGTGTGTGTGTGTGTGT 1077
DB 110553 CGTGGCAGAGTGTCTCTGTGGCAGGCGCGTGGGTGTATAGGTGTGTGTGTGTGTGTGT 110612
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DB 110613 CGGACACAGCTGTAGCCGAGAGAGAGGTTCACTTGTGTGTGTGTGTGTGTGTGTGT 110672
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QY 1317 GATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1353
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Job time : 5132.03 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 18:41:41 ; Search time 396.318 Seconds
(without alignments)
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Title: US-09-692-077D-1

Perfect score: 1353
Sequence: 1 atgacaccacagaccacca.....ggaccacagcgcgcgtga 1353

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353	100.0	1353	23	AA199905 Human alpha-2BAR t
2	1351.4	99.9	1353	22	AD04762 Human alpha2B-adre
3	1351.4	99.9	1353	24	AD044389 Human alpha-2B-adr
4	1349.8	99.8	2072	25	ACA56583 Human signalling p
5	1349.8	99.8	3274	25	AB242624 Human alpha 2b-adr
6	1330.6	98.3	2064	12	AAQ14151 Human alpha 2 beta
7	1330.6	98.3	2064	18	AAT59499 Human alpha-2b adr
8	1325	97.9	1344	23	AA199906 Human alpha-2BAR t

9	1323.4	97.8	1344	22	AD04761 Human alpha2B-adre
10	1323.4	97.8	1344	24	AD44388 Human alpha-2B-adr
11	600.2	44.4	6904	24	AB132075 Human immune syste
12	600.2	44.4	6904	24	AD28365 Human chemically t
13	512.6	37.9	6904	24	AB132074 Human immune syste
14	512.6	37.9	6904	24	AD28364 Human chemically t
15	448.8	33.2	1383	23	AA19931 Human alpha-2CAR e
16	447.2	33.1	2826	25	AB242625 Human alpha 2c-adr
17	444	32.8	1382	15	AA064890 Human derived adre
18	444	32.8	1382	24	AB235643 Human gene express
19	444	32.8	1382	25	ACA56558 Human signalling p
20	443	32.7	1350	23	AA19918 Human alpha-2BAR v
21	442.4	32.7	3653	25	AB242623 Human alpha 2a-adr
22	441.4	32.6	1350	23	AA19917 Human alpha-2BAR v
23	437.6	32.3	1371	23	AA19933 Human signalling p
24	430	31.8	3604	25	ACA56582 Human gene express
25	293.6	21.7	1758	24	AB235339 Human chemically t
26	262.6	19.4	1733	24	AB047500 Human chemically t
27	262.6	19.4	1733	24	AB047501 Human chemically t
28	262.6	19.4	7353	24	AB132073 Human immune syste
29	262.6	19.4	7353	24	AD28363 Human chemically t
30	262.4	19.4	4850	24	AD28395 Human chemically t
31	210.4	15.6	1140	18	AAT88392 Human immune syste
32	184.8	13.7	3125	23	ABU13003 Drosophila melanog
33	184.8	13.7	3335	13	AAQ21928 Drosophila melanog
34	183.2	13.5	6313	23	ABU13002 Oligonucleotide fo
35	181.4	13.4	1733	24	AB047498 Human chemically t
36	181.4	13.4	1733	24	AB047499 Human chemically t
37	181.4	13.4	7353	24	ABU13002 Human immune syste
38	181.4	13.4	7353	24	AD28362 Human chemically t
39	171	12.6	1431	18	AAT85635 Human chemically t
40	165.8	12.3	4850	24	AD28394 Human chemically t
41	158.6	11.7	921	15	AA072224 Human alpha-1B adr
42	158.6	11.7	921	16	AAT11608 Human alpha-1B adr
43	158.6	11.7	1567	15	AA087879 Human/rat alpha-1B
44	158.6	11.7	1567	16	AAT11615 Human/rat hybrid a
45	158.6	11.7	1738	15	AA062817 Genomic sequence e

ALIGNMENTS

RESULT 1	AA199905 standard; DNA; 1353 BP.
ID	AA199905
AC	AA199905;
XX	XX
DT	18-FEB-2002 (first entry)
XX	XX
DE	Human alpha-2BAR third intracellular loop encoding DNA.
XX	XX
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2BAR;
KW	Genbank Accession AF009500; chromosome 2; ds.
OS	Homo sapiens.
XX	XX
FH	Key
FT	CDS
FT	1..1353
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "alpha-2BAR"
FT	/note= "sequence includes a 9 nucleotide polymorphic site
FT	at nucleotides 901-909 absent in the alpha-2BAR
FT	variant (AA199906)"
PN	MO200179561-A2.
XX	XX
PD	25-OCT-2001.
XX	XX
PF	17-APR-2001; 2001WO-US12575.

XX 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI: 2001-611728/70.
DR P-FSDB; AAM52117.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX
XX Claim 4; Page 144; 163pp; English.

XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C, or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (999cggggccg) or (B) (999cgggctgg) at
CC positions 961-972 of (IIIV). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline (e.g. UK14304), BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the third intracellular loop of
CC the human alpha-2BAR (Genbank Accession AF009500), the sequence includes
CC a 9 nucleotide polymorphic site at nucleotides 901-909, absent in the
CC alpha-2BAR variant (AA199906).
XX
XX Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 other;

Query Match 100.0%; Score 1353; DB 23; Length 1353;
Best Local Similarity 100.0%; Pred. No. 9, 1e-258;
Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCAACCAAGAGCCCTACTCCGTGAGAGCCACAGCCGACATAGAGCGGACATCAC 60
DB 1 ATGACCAACCAAGAGCCCTACTCCGTGAGAGCCACAGCCGACATAGAGCGGACATCAC 60
QY 61 TTCCCTATTCTCTTAAACATCTTGGCAAGCTGTGATCTGTGGTGTGAACAGC 120
DB 61 TTCCCTATTCTCTTAAACATCTTGGCAAGCTGTGATCTGTGGTGTGAACAGC 120
QY 121 CGCTGCTGCGGCGCCCTCAGAACTGTCTGTGCTGTGGCGCGCGGACATCTCTG 180
DB 121 CGCTGCTGCGGCGCCCTCAGAACTGTCTGTGCTGTGGCGCGCGGACATCTCTG 180
QY 181 GTGGCCAGCCTCATCATCTCTTCTGTGAGCAAGAGCTGTGGGCTAAGTACTTTC 240
DB 181 GTGGCCAGCCTCATCATCTCTTCTGTGAGCAAGAGCTGTGGGCTAAGTACTTTC 240
QY 241 CGGCGCAGTGTGAGAGGTGTAAGTGTGGGCTGTGACGTCTTTCTGTGACCTGTGCATC 300
DB 241 CGGCGCAGTGTGAGAGGTGTAAGTGTGGGCTGTGACGTCTTTCTGTGACCTGTGCATC 300
QY 301 GTGCACTGTGCGCATCAGCTGAGACGCTACTGAGCGGTGAGCCGCGCGCTGAGTAC 360

DB 301 GTGCACTGTGCGCATCAGCTGAGACGCTACTGAGCGGTGAGCCGCGCTGAGTAC 360
QY 361 AACTCAAGGAGACCCCGCGGACATCAAGTCAATCATCTGATGTGCTCATCGCC 420
DB 361 AACTCAAGGAGACCCCGCGGACATCAAGTCAATCATCTGATGTGCTCATCGCC 420
QY 421 GCGGTATCTGCTGTGCGGCGCCCTCATCTAAGAGGCGACAGAGGCGCCGCGG 480
DB 421 GCGGTATCTGCTGTGCGGCGCCCTCATCTAAGAGGCGACAGAGGCGCCGCGG 480
QY 481 CGCCCCAGTGAAGTGAACCAAGAGAGCTGTGATCTGTGCTTCCAGCATCGAATC 540
DB 481 CGCCCCAGTGAAGTGAACCAAGAGAGCTGTGATCTGTGCTTCCAGCATCGAATC 540
QY 541 TTCTTGTCTCTGTGCTCATCATGATCTGTGCTGCTGCGCATCTTACCTGACCAA 600
DB 541 TTCTTGTCTCTGTGCTCATCATGATCTGTGCTGCTGCGCATCTTACCTGACCAA 600
QY 601 CGCAGCAACCGCAAGGTCCAGGCGCAAGGCGGCGCTGAGGAGTCCAGAGCAG 660
DB 601 CGCAGCAACCGCAAGGTCCAGGCGCAAGGCGGCGCTGAGGAGTCCAGAGCAG 660
QY 661 CCCGACCGGACCAATGTGAGGCTTTGGGCTTCAAGCAATGCGGACCCCTGCTTGTG 720
DB 661 CCCGACCGGACCAATGTGAGGCTTTGGGCTTCAAGCAATGCGGACCCCTGCTTGTG 720
QY 721 GCTTGTGCAAGAGTCAAGCACTGAGAGTCACTGAGGAGAGAGAGAGAGAGAG 780
DB 721 GCTTGTGCAAGAGTCAAGCACTGAGAGTCACTGAGGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTGAAGTATCTGGAGACCCGCGCTTGGCCACCCAGTTGGCTGCTTCCAACTCA 840
DB 781 ACCCTGAAGTATCTGGAGACCCGCGCTTGGCCACCCAGTTGGCTGCTTCCAACTCA 840
QY 841 GGCAGGCGCAGAGAGAGGCTTTGTGAGGCACTCTCAAGAGATGAAGTGAAGAGAG 900
DB 841 GGCAGGCGCAGAGAGAGGCTTTGTGAGGCACTCTCAAGAGATGAAGTGAAGAGAG 900
QY 901 GAAAG 960
DB 901 GAAAG 960
QY 961 TCAGCTTGAAGCGCCCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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QY 1021 GGCAGGCTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 GGCAGGCTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 GCGAGAGTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 GCGAGAGTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
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DB 1141 GTGCTGTGAGTCT 1200
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QY 1321 CTGTGCGCGCGGTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1353
DB 1321 CTGTGCGCGCGGTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1353

RESULT 2

AD04762
ID AD04762 standard; DNA; 1353 BP.
XX
AC AD04762;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX
KW Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW norepinephrine; epinephrine; therapy; vascular contraction;
KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant; de.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /*tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT protein"
XX
PN WO200129082-A1.
XX
PD 26-APR-2001.
XX
PF 20-OCT-2000; 2000WO-FI00913.
XX
PR 22-OCT-1999; 99US-0422985.
XX
PA (JUVA-) JUVAANTIA PHARMA LTD OY.
XX
PI Snapiir A, Heinonen P, Alhopuro P, Karonen M, Koulou M, Pesonen U;
PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyssönen K;
PI Salonen R, Kaahenen J, Valkonen V;
XX
DR MPI; 2001-300318/31.
XX
P-PSDB; AAE00990.
XX
PT New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular
PT loop of the polypeptide, for treating vascular contraction of coronary
PT arteries -
XX
PS Disclosure; Page 27-29; 37pp; English.
XX
CC The present sequence is a gene encoding human alpha2B-adrenoceptor
CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
CC acids (amino acids 294-311), located in the third intracellular loop of
CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
CC Alpha2-AR mediate many of the physiological effects of the
CC catecholamines, norepinephrine and epinephrine. An antagonist of
CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
CC vascular contraction of coronary arteries and a disease involving
CC vascular contraction of coronary arteries which is clinically expressed
CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
CC clinically expressed as Prinzmetal's variant form or acute myocardial
CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
XX
SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;

DB 61 TTCCTCATCTCTTTACATCTTGGCAAGCTCTGATCATCTGCTGTGTACACAGC 120
QY CGCTGCTGGGCGCCCTGAGAACCTGTTCTGATGCTGGGCGCGCGGACATCTG 180
DB 121 CGCTGCTGGGCGCCCTGAGAACCTGTTCTGATGCTGGGCGCGCGGACATCTG 180
QY 181 GTGGCAGCCTCATCTATCTCTTCTGCTGGCCAGCAGCTGTGGGCTACTGTGTTCT 240
DB 181 GTGGCAGCCTCATCTATCTCTTCTGCTGGCCAGCAGCTGTGGGCTACTGTGTTCT 240
QY 241 CGGCGCAGCTGTGGGAGGTTGTTCTGCTGGGCTGTGAGTGTCTTCTGACCTGTGATC 300
DB 241 CGGCGCAGCTGTGGGAGGTTGTTCTGCTGGGCTGTGAGTGTCTTCTGACCTGTGATC 300
QY 301 GTGGCAGCCTCATCTATCTCTTCTGCTGGCCAGCAGCTGTGGGCTACTGTGTTCT 360
DB 301 GTGGCAGCCTCATCTATCTCTTCTGCTGGCCAGCAGCTGTGGGCTACTGTGTTCT 360
QY 361 AACTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 420
DB 361 AACTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 420
QY 421 GCGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 GCGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 CGCCCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 540
DB 481 CGCCCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 540
QY 541 TTCTTGTCTCTTGTCTCTTGTCTCTTGTCTCTTGTCTCTTGTCTCTTGTCTCTTGTCTCT 600
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QY 601 CGCAGCAACCGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 660
DB 601 CGCAGCAACCGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 660
QY 661 CCCCCAGCAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 720
DB 661 CCCCCAGCAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 720
QY 721 GCTTGTGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 780
DB 721 GCTTGTGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 780
QY 781 ACCCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 840
DB 781 ACCCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 840
QY 841 GGCAGAGGCGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 900
DB 841 GGCAGAGGCGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 900
QY 901 GAAAG 960
DB 901 GAAAG 960
QY 961 TCAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1020
DB 961 TCAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1020
QY 1021 GGCAGAGTGTCTCTGAG 1080
DB 1021 GGCAGAGTGTCTCTGAG 1080
QY 1081 GGCAGAGTGTCTCTGAG 1140
DB 1081 GGCAGAGTGTCTCTGAG 1140
QY 1141 GTGCTGTGAGTGTCTCTGAG 1200
DB 1141 GTGCTGTGAGTGTCTCTGAG 1200

QY 1201 TCGAAGTGGCCCATGAGCCTCTTCCAGTTCTTCTGATGCGGCTACTGCAACAGCTCA 1260
DB 1201 TCGAAGTGGCCCATGAGCCTCTTCCAGTTCTTCTGATGCGGCTACTGCAACAGCTCA 1260
QY 1261 CTGAACCTGTTATCTTACACCATCTTCAACAGAGCTTCGCGCGTCTTCGCGAGATC 1320
DB 1261 CTGAACCTGTTATCTTACACCATCTTCAACAGAGCTTCGCGCGTCTTCGCGAGATC 1320
QY 1321 CTGTGCGCGCGCTGAGACCCAGAGCGGCTGTGA 1353
DB 1321 CTGTGCGCGCGCTGAGACCCAGAGCGGCTGTGA 1353
RESULT 3
AD44389
ID AAD44389 standard; DNA; 1353 BP.
AC AAD44389;
XX
XX 13-DEC-2002 (first entry)
DT 13-DEC-2002 (first entry)
XX
XX Human alpha-2B-adrenoceptor gene.
DE Human alpha-2B-adrenoceptor gene.
XX
XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KM hypertension; hypotensive; gene; de.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..1353
FT CDS /tag= a
FT /product= "Human alpha-2B-adrenoceptor protein"
FT
XX WO200266617-A1.
XX
XX 29-AUG-2002.
PD
XX 13-FEB-2002; 2002MO-FI00113.
PF
XX 20-FEB-2001; 2001FI-0000323.
PR
XX (JURI-) JURILAB LTD OY.
PA
XX Salonen J;
PI
XX MPI; 2002-667063/71.
DR P-PSDB; AAE26634.
DR
XX
XX Detecting a risk of hypertension and targeting treatment in a subject
PT by determining the pattern of alleles encoding a variant
PT alpha-2-adrenoceptor -
XX
XX Disclosure; Page 27-29; 35pp; English.
XX
XX The invention relates to a method for detecting a risk of hypertension
CC by determining the pattern of alleles encoding a variant alpha-2B-
CC adrenoceptor (AR) protein. The methods and compositions of the invention
CC are useful for detecting risks and targeting treatment for hypertension.
CC The kit is also useful for selecting for clinical drug trials testing
CC the antihypertensive effect of compounds. The present sequence is human
CC alpha-2B-adrenoceptor gene.
XX
XX Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
SQ
Query Match 99.9%; Score 1351.4; DB 24; Length 1353;
Best Local Similarity 99.9%; Pred. No. 1.9e-257;
Matches 1353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGACCAACAGAGACCCCTTCTCTGTCAGAGCCAGCGGCTATGAGGCGGCATCACC 60
DB 1 ATGAGACCAACAGAGACCCCTTCTCTGTCAGAGCCAGCGGCTATGAGGCGGCATCACC 60

QY 61 TTCTCATTTCTCTTTACCATCTTTCGCAACGCTCTGCTATCTGCGTGTGACCAAC 120
DB 61 TTCTCATTTCTCTTTACCATCTTTCGCAACGCTCTGCTATCTGCGTGTGACCAAC 120
QY 121 CGCTGCTGCGGCGCCCTTCAGAACTGTTCTCTGCTGTGCTGTGCGCGCGGCAATCTCG 180
DB 121 CGCTGCTGCGGCGCCCTTCAGAACTGTTCTCTGCTGTGCTGTGCGCGCGGCAATCTCG 180
QY 181 GTGGCAGAGCTCATGCTCTTCTCTGCTGCGCAACAGCTCTGCGGCTACTGCTACTTC 240
DB 181 GTGGCAGAGCTCATGCTCTTCTCTGCTGCGCAACAGCTCTGCGGCTACTGCTACTTC 240
QY 241 CGGCGCAGCTGTGCGAGGTGTACTGTGCGCTGACAGTCTTCTTGCACCTGCTCATC 300
DB 241 CGGCGCAGCTGTGCGAGGTGTACTGTGCGCTGACAGTCTTCTTGCACCTGCTCATC 300
QY 301 GTGCACCTGTGTGCGCATCAGCTTGAACCGCTTACTGTGAGCCGCGGCTGAGATAC 360
DB 301 GTGCACCTGTGTGCGCATCAGCTTGAACCGCTTACTGTGAGCCGCGGCTGAGATAC 360
QY 361 AACTCCAGCGGACCGCGCGCGCATCAAGTGCATCATCTGCTGCTGCTCATCGCC 420
DB 361 AACTCCAGCGGACCGCGCGCGCATCAAGTGCATCATCTGCTGCTGCTCATCGCC 420
QY 421 GCGCTCATCTGCTGCGCGCGCATCAAGTGCATCAAGGCGGACGAGCGCGCGCGG 480
DB 421 GCGCTCATCTGCTGCGCGCGCATCAAGTGCATCAAGGCGGACGAGCGCGCGCGG 480
QY 481 CGGCGCGCATGCAAGCTCAACAGAGGCTGTGATCTTGTGCTTCCAGCATCGGATCT 540
DB 481 CGGCGCGCATGCAAGCTCAACAGAGGCTGTGATCTTGTGCTTCCAGCATCGGATCT 540
QY 541 TTCTTGTGCTCTTGTGCTCATGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 TTCTTGTGCTCTTGTGCTCATGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CGCAGCAACCGCAGAGGTCCAGGCGCAAGGCGGCGCTGCGCAGGATGCTCAAGCAG 660
DB 601 CGCAGCAACCGCAGAGGTCCAGGCGCAAGGCGGCGCTGCGCAGGATGCTCAAGCAG 660
QY 661 CCCCGACCGACATGCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 CCCCGACCGACATGCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GCTTGTGCGAGAGGTCAACGCACTGCAAGTCCACTGCGGAGAGAGAGAGAGAGAGAG 780
DB 721 GCTTGTGCGAGAGGTCAACGCACTGCAAGTCCACTGCGGAGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTGAAAGATATGAGGACCGGCGCTTGCACACCAAGTTGAGGCTTCCCACTCA 840
DB 781 ACCCTGAAAGATATGAGGACCGGCGCTTGCACACCAAGTTGAGGCTTCCCACTCA 840
QY 841 GGCAGAGGCGCAAGAGAGGTGTTGTGCGGCTTCCAGAGAGTAACTGAAGAGAG 900
DB 841 GGCAGAGGCGCAAGAGAGGTGTTGTGCGGCTTCCAGAGAGTAACTGAAGAGAG 900
QY 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGTGAACCCAGAGCAAGTGTCTCGGCGC 960
DB 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGTGAACCCAGAGCAAGTGTCTCGGCGC 960
QY 961 TCAAGCTTGAAGCCCGCGCTGAGCAGCAGAGGCTCCCGGCTGTGCGCACCTTACCT 1020
DB 961 TCAAGCTTGAAGCCCGCGCTGAGCAGCAGAGGCTCCCGGCTGTGCGCACCTTACCT 1020
QY 1021 GGCAGAGTCTCTTGTGCGCAGGCGCTGTGCTGCTAATGAGTGTGAGTGTGCTGCAAG 1080
DB 1021 GGCAGAGTCTCTTGTGCGCAGGCGCTGTGCTGCTAATGAGTGTGAGTGTGCTGCAAG 1080
QY 1081 GGCAGAGTACCCGAGAGAGAGGCTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 GGCAGAGTACCCGAGAGAGAGGCTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 GTGCTGTGCTGCTTCCCTTCTTCTTCACTCAAGCTTGTGCGGCTGCTGCGGAGCAG 1200

|||||
DB 1141 GTGCTGTGCTGTCCCTCTCTCTCAGCTACAGCTGGGCCCATCTGCGGAAGCAC 1200
QY 1201 TGCAGGTGCGCCATGAGCCCTCTCCAGTCTCTTGTGATGGGCTACAGCAACACTCA 1260
DB 1201 TGCAGGTGCGCCATGAGCCCTCTCCAGTCTCTTGTGATGGGCTACAGCAACACTCA 1260
QY 1261 CTGAACCTGTATCTACACATCTTCAACAGAGCTTCGCGCGTCTTCCGGAAGATC 1320
DB 1261 CTGAACCTGTATCTACACATCTTCAACAGAGCTTCGCGCGTCTTCCGGAAGATC 1320
QY 1321 CTGTGCGCGCGGTGAGCCAGACGCGCTGTGA 1353
DB 1321 CTGTGCGCGCGGTGAGCCAGACGCGCTGTGA 1353

RESULT 4
ACAS6583
ID ACAS6583 standard; cDNA; 2072 BP.
XX
XX ACAS6583;
AC 06-JUN-2003 (first entry)
XX
DT Human signalling pathway polynucleotide probe SEQ ID NO 1181.
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1181.
XX
XX Human; probe; ss; array element; Parkinson's disease;
KM signalling pathway population; cancer; adenocarcinoma; leukaemia;
KM Immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
OS Homo sapiens.
XX
PN US6500938-B1.
XX
XX 31-DEC-2002.
PD
PF 30-JAN-1998; 98US-0016434.
XX
PR 30-JAN-1998; 98US-0016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JI;
XX
XX WPI: 2003-352189/33.
DR
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides -
XX
XX Claim 1, SEQ ID NO 1181; 65pp; English.
XX
XX The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signalling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia;
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO

CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.
XX
XX Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 other;
SQ
Query Match 99.8%; Score 1349.8; DB 25; Length 2072;
Best Local Similarity 99.9%; Pred. No. 4,1e-257;
Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGACACACAGGAGACCCCTACTCCGTCAGAGGACAGCGGACCATPACGGGCGGATCAC 60
DB 413 ATGACACACAGGAGACCCCTACTCCGTCAGAGGACAGCGGACCATPACGGGCGGATCAC 472
QY 61 TTCCTCATCTCTTTACATCTTCGCAACGCTCTGATCATCTGCTGTGTGACAG 120
DB 473 TTCCTCATCTCTTTACATCTTCGCAACGCTCTGATCATCTGCTGTGTGACAG 532
QY 121 CGCTGCTGTGCGGCGGCGGCTGAGAACTGTTCCTGTGTCTGCTGCGCGCGGCGGATCTG 180
DB 533 CGCTGCTGTGCGGCGGCGGCTGAGAACTGTTCCTGTGTCTGCTGCGCGCGGCGGATCTG 592
QY 181 GTGGCCAGGCTCATCATCCCTTCTGCTGCGGCAAGAGCTGTGGCTTACGTATCTTC 240
DB 593 GTGGCCAGGCTCATCATCCCTTCTGCTGCGGCAAGAGCTGTGGCTTACGTATCTTC 652
QY 241 CGGCGACGCTGTGCGAGGTGTACCTGCGCTGACAGTCTCTTGTGACCTGTGTCATC 300
DB 653 CGGCGACGCTGTGCGAGGTGTACCTGCGCTGACAGTCTCTTGTGACCTGTGTCATC 712
QY 301 GTGACCTGTGTGCGCATCAGCCTGAGCGGCTACTGTGGCGGTGAGCGGCGCTGAGATAC 360
DB 713 GTGACCTGTGTGCGCATCAGCCTGAGCGGCTACTGTGGCGGTGAGCGGCGCTGAGATAC 772
QY 361 AACTCCAAAGCGACCCCGGCGGCGCATCAAGTGCATATCTCACTGTGTGCTCATCGCC 420
DB 773 AACTCCAAAGCGACCCCGGCGGCGCATCAAGTGCATATCTCACTGTGTGCTCATCGCC 832
QY 421 GCCGTATCTGCTGCGGCGGCGGCTCATCTCAAGAGGCGACAGAGGCGGCGGCGGCGG 480
DB 833 GCCGTATCTGCTGCGGCGGCGGCTCATCTCAAGAGGCGACAGAGGCGGCGGCGGCGG 892
QY 481 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
DB 893 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 952
QY 541 TTCCTTGTCTCTTGTCTCATCATGATCTTGTCTTACTGCGCATCTACTGATCGCAAA 600
DB 953 TTCCTTGTCTCTTGTCTCATCATGATCTTGTCTTACTGCGCATCTACTGATCGCAAA 1012
QY 601 CGAGCAACCGAGAGGTCCAGAGGCGCAAGAGGAGGCGGCGGCGGCGGCGGCGGCGG 660
DB 1013 CGAGCAACCGAGAGGTCCAGAGGCGCAAGAGGAGGCGGCGGCGGCGGCGGCGGCGG 1072
QY 661 CCCGACCCGACCATGATGAGGCGCTTGTGCTGAGCCAACTGACGCGCTGTGTG 720
DB 1073 CCCGACCCGACCATGATGAGGCGCTTGTGCTGAGCCAACTGACGCGCTGTGTG 1132
QY 721 GCTTGTGCGAGAGGTCAACGACACTGAAAGTCCATCTGCGGAGAGAGAGAGAGGAG 780
DB 1133 GCTTGTGCGAGAGGTCAACGACACTGAAAGTCCATCTGCGGAGAGAGAGAGAGAGG 1192
QY 781 ACCCGTGAAGATCTAGGAGCCGCGGCGTTCGACCCAGTGTGGGCTGCTCCCACTCA 840
DB 1193 ACCCGTGAAGATCTAGGAGCCGCGGCGTTCGACCCAGTGTGGGCTGCTCCCACTCA 1252
QY 841 GCGCAGGCGCAGAGAGGAGGTGTTGTGCGGATCTTCAGAGGATGAAGAGAGAG 900
DB 1253 GCGCAGGCGCAGAGAGGAGGTGTTGTGCGGATCTTCAGAGGATGAAGAGAGAG 1312
QY 901 GAAAG 960
DB 1313 GAAAG 1372
QY 961 TCAGCTTGAGGCGGCGGCGTGTGAGGAGCAAGAGGCTCCGCGGTGTGCGACCCCTACGT 1020


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QY 601 CCGAGCAACCGCAGAGCTCCCAAGGCGCCAAAGGGGGGCTTGGGCGAGGTGATCCAAACAG 660
DB 601 CCGAGCAACCGCAGAGCTCCCAAGGCGCCAAAGGGGGGCTTGGGCGAGGTGATCCAAACAG 660
QY 661 CCCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 661 CCCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 GCTTCTGAGAGAGGATCAACGCACTGGAAGTCCAGTGGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 721 GCTTCTGAGAGAGGATCAACGCACTGGAAGTCCAGTGGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 ACCCTTGAAGATCTGGGAGCCCGGGGCTTGGCAACCCAGTGGGCTGCTTCCCACTCA 840
DB 781 ACCCTTGAAGATCTGGGAGCCCGGGGCTTGGCAACCCAGTGGGCTGCTTCCCACTCA 840
QY 841 GGGCAGGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 GGGCAGGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 TCAGCTTGGAGCCCGGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1020
DB 961 TCAGCTTGGAGCCCGGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1020
QY 1021 GGGCAGAGTCTCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
DB 1021 GGGCAGAGTCTCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1081 GGGCAGAGTCTCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 GGGCAGAGTCTCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GTGCTCTGCTGAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
DB 1141 GTGCTCTGCTGAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
QY 1201 TGCAGAGTGGCCCATGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
DB 1201 TGCAGAGTGGCCCATGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
QY 1261 CTGAACCTCTGATCTCAACACATCTTCAACACAGAGATTCGCGCGTCTTCCGAGAGATC 1320
DB 1261 CTGAACCTCTGATCTCAACACATCTTCAACACAGAGATTCGCGCGTCTTCCGAGAGATC 1320
QY 1321 CTGTGCGGCGCTGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCG 1353
DB 1321 CTGTGCGGCGCTGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCG 1353

RESULT 6
AAQ14151
ID AAQ14151 standard; DNA; 2064 BP.
XX
XX AAQ14151;
XX
XX 06-JAN-1992 (first entry)
XX
XX Human alpha 2 beta adrenergic receptor gene.
XX
XX Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 288..1752
XX FT /tag= a
XX
XX US0503337-A.
```

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PD 01-OCT-1991.
XX
XX 30-OCT-1989; 89US-0428856.
XX
XX 30-OCT-1989; 89US-0428856.
XX
XX (NEUR-) NEUROGENETIC CORP.
XX
XX Weinshank RL, Hartig PR;
XX
XX WPI, 1991-310087/42.
XX
XX P-PSDB; AARI4149.
XX
XX Isolated DNA encoding human adrenergic receptor - for detecting
XX PT nucleic acids encoding alpha, 2-beta adrenergic receptor, for
XX PT screening drugs.
XX
XX Claim 1; Fig 2; 15pp; English.
XX
XX Clone NGC-alpha2beta was isolated from a human spleen genomic
XX CC library by screening with a fragment of the human 5-HT1A receptor
XX CC gene. The gene can be used to express recombinant receptor protein
XX CC which can be used to produce antibodies for inhibition of receptor
XX CC function.
XX
XX Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
XX
XX Query Match 98.3%; Score 1330.6; DB 12; Length 2064;
XX Best Local Similarity 99.0%; Pred. No. 2,5e-253;
XX Matches 1339; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX
QY 1 ATGAGCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 399 ATGAGCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 458
QY 61 TTCCTATCTCTTACATCTTGGCAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 120
DB 459 TTCCTATCTCTTACATCTTGGCAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 518
QY 121 CGCTGCTGCGGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 519 CGCTGCTGCGGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
QY 181 GTGGCAGGCTATATCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 579 GTGGCAGGCTATATCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 638
QY 241 CGGCGCAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 639 CGGCGCAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 698
QY 301 GTGACCTGTGGCATCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 699 GTGACCTGTGGCATCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 758
QY 361 AACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 759 AACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 818
QY 421 GCGCTATCTGCTGCGGCGGCTGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 819 GCGCTATCTGCTGCGGCGGCTGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 878
QY 481 GCGCCCAAGTGAAGCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 879 GCGCCCAAGTGAAGCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 938
QY 541 TTCTTTGCTCTTGGCTATATGATCTTGTCTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 939 TTCTTTGCTCTTGGCTATATGATCTTGTCTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 998
QY 601 CCGAGCAACCGCAGAGTCCCAAGGCGCCAAAGGGGGGCTTGGGCGAGGTGATCCAAACAG 660
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Db 999 CCGAGCAACCGCAGAGGTCCAGAGGCCAAGGGGGGCTGGGAGGATGATCCAGCAG 1058
Qy 661 CCCCGACCCGACCATGTGGGGCTTTGAGCTCAAGCCAACTGCCAGCTTGTGTG 720
Db 1059 CCCCGACCCGACCATGTGGGGCTTTGAGCTCAAGCCAACTGCCAGCTTGTGTG 1118
Qy 721 GCTTCTGCAGAGAGGTCAACGCACTGGAAGTCCACTGGGAGAAAGAGAGGGGGAG 780
Db 1119 GCTTCTGCAGAGAGGTCAACGCACTGGAAGTCCACTGGGAGAAAGAGAGGGGGAG 1178
Qy 781 ACCCTGGAAGATCTGAGAACCCGGGCTTGCACCCAGTGGGCTGCTCCCTCAACTCA 840
Db 1179 ACCCTGGAAGATCTGAGAACCCGGGCTTGCACCCAGTGGGCTGCTCCCTCAACTCA 1238
Qy 841 GGCAGAGGCGCAGAGAGGGGTGTTGTGGGCACTCTCAAGAGTAACTGAAGAGAG 900
Db 1239 GGCAGAGGCGCAGAGAGGGGTGTTGTGGGCACTCTCAAGAGTAACTGAAGAGAG 1298
Qy 901 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 1299 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1358
Qy 961 TCAGCTTGACAGCCCGCTGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 1359 TCAGCTTGACAGCCCGCTGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1418
Qy 1021 GGCAGAGTCTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1419 GGCAGAGTCTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1478
Qy 1081 GGCAGAGTCTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1479 GGCAGAGTCTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1538
Qy 1141 GTGCTGTGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
Db 1539 GTGCTGTGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1598
Qy 1201 TGCAGAGTGCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
Db 1599 TGCAGAGTGCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1658
Qy 1261 CTGAACCTCTTATCTACACCATCTTCAACAGAGACTTCGCGGTGCTTCCGAGAGATC 1320
Db 1659 CTGAACCTCTTATCTACACCATCTTCAACAGAGACTTCGCGGTGCTTCCGAGAGATC 1718
Qy 1321 CTGTGCGCGCCGTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1353
Db 1719 CTGTGCGCGCCGTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1751

RESULT 7
AAT59499
ID AAT59499 standard; DNA; 2064 BP.
XX
AC AAT59499;
XX
AC 25-MAR-2003 (updated)
XX
DT 06-MAY-1997 (first entry)
XX
DE Human alpha-2b adrenergic receptor genomic DNA clone.
XX
KW Alpha-2b adrenergic receptor; adrenoceptor; adrenal line;
XX
KW epinephrine; signal transduction; neurotransmitter; ligand; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
XX CDS 288..1751
XX FT /*tag= a
XX PN
XX US595880-A.
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PD 21-JAN-1997.
XX
PF 22-OCT-1992; 92US-0965040.
XX
PR 30-OCT-1989; 89US-0428856.
XX 30-MAY-1991; 91US-0707604.
PR 22-OCT-1992; 92US-0965040.
XX
PA (SYMA-) SYNAPTRIC PHARM CORP.
XX
PI Hartig PR, Weinschenk RL;
XX WPI; 1997-107576/10.
XX P-PSDB; AAM11804.
XX
PT Assay for alpha-2b adrenergic receptor ligands - using membranes of
XX cells expressing recombinant receptor
XX
PS Disclosure; Fig 2A-E; 16pp; English.
XX
CC A genomic DNA clone (AAT59499) codes for human alpha-2b adrenergic
CC receptor (AAM11804), a member of the rhodopsin-like signal transducer
CC family. It was isolated from a human spleen genomic library in the
CC lambda vector Charon 28 by screening with a 1.6 kb fragment of the
CC human 5-hydroxytryptamine receptor gene. Plasmid pNc-alpha-2b
CC comprising DNA encoding the alpha-2b adrenoceptor is deposited as
CC ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2b
CC adrenoceptor in bacterial, yeast or mammalian cells; transfected
CC Ltk- cells, designated L-Nc-alpha-2b, are deposited as ATCC CRL
CC 10275. Membranes of such cells can used in novel methods to
CC identify drugs which specifically interact with, and bind to, the
CC alpha-2b adrenergic receptor.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 2064 BP; 319 A; 636 C; 659 G; 390 T; 0 other;
XX
Query Match 98.3%; Score 1330.6; DB 18; Length 2064;
Best Local Similarity 99.0%; Pred. No. 2,5e-253;
Matches 1339; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 AAGGACACACAGAGACCCCTTCTCTGAGAGGCGCAAGAGGCGGCGGCGCATCAC 60
Db 399 ATGAGACACACAGAGACCCCTTCTCTGAGAGGCGCAAGAGGCGGCGGCGCATCAC 458
Qy 61 TTCCCATCTCTTTTACCATCTTGGCAAGCTGTGATCTGATCTGTGATCTGATCTG 120
Db 459 TTCCCATCTCTTTTACCATCTTGGCAAGCTGTGATCTGATCTGTGATCTGATCTG 518
Qy 121 CGCTGCTGCGGCGCCCTTCAAGACCTGTTCTGTGTGCTGTGCGCGCGCGCATCTCG 180
Db 519 CGCTGCTGCGGCGCCCTTCAAGACCTGTTCTGTGTGCTGTGCGCGCGCGCATCTCG 578
Qy 181 GTGGCCAGGCTCATCATCTCTTCTGCGGCAAGAGCTGTGGGCTGATGATCTG 240
Db 579 GTGGCCAGGCTCATCATCTCTTCTGCGGCAAGAGCTGTGGGCTGATGATCTG 638
Qy 241 CGGCGACGTGTGAGAGGTGATCTGCGCTGAGAGTGTCTTCTGCACTCTGTTCATC 300
Db 639 CGGCGACGTGTGAGAGGTGATCTGCGCTGAGAGTGTCTTCTGCACTCTGTTCATC 698
Qy 301 GTGACACTGTGCGCATCAAGCTTGACCGCTTCTGAGAGGCGGCGGCTGAGATAC 360
Db 699 GTGACACTGTGCGCATCAAGCTTGACCGCTTCTGAGAGGCGGCGGCTGAGATAC 758
Qy 361 AATTCAGAGCGACCCCGCGCGCATCAAGTGTATCTCACTGATGAGTGTGATCTG 420
Db 759 AATTCAGAGCGACCCCGCGCGCATCAAGTGTATCTCACTGATGAGTGTGATCTG 818
Qy 421 GCGGTATCTGCTGCGCGCCCTCATCTCAAGAGGCGACAGGCGCGCGCGCGCGCG 480
Db 819 GCGGTATCTGCTGCGCGCCCTCATCTCAAGAGGCGACAGGCGCGCGCGCGCGCG 878
Qy 481 CGCCCCAGTGAAGTCAACAGAGAGGCGGTGTATCTCTGCGCTTCAGATCGATCT 540
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879 CGCCCCAGTGCAGACGAGAGGCTGTATCATCTGCGCTCCAGCATCGGATCT 938
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601 CCAGCAACCCGAGAGAGTCCCAAGGCGGCGCTTGGCGAGGGTGAATCCAGCAG 660
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999 CCAGCAACCCGAGAGAGTCCCAAGGCGGCGCTTGGCGAGGGTGAATCCAGCAG 1058
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661 CCCCCAGCCGACCATGTGTGGGCTTTGGCTCTAGCCAACTGCGAGCCCTTGGCTGTG 720
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1059 CCCCCAGCCGACCATGTGTGGGCTTTGGCTCTAGCCAACTGCGAGCCCTTGGCTGTG 1118
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721 GCTTCTGCGAGAGAGTCAACCGACACTGGAAGTCCACTGGGAGAAAGAGAGGGGAG 780
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1119 GCTTCTGCGAGAGAGTCAACCGACACTGGAAGTCCACTGGGAGAAAGAGAGGGGAG 1178
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781 ACCCTGGAAGATTAAGTGGGACCCGCGGCTTGGCGACCCAGTGTGGGCTGCTTCCCACTGA 840
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1179 ACCCTGGAAGATTAAGTGGGACCCGCGGCTTGGCGACCCAGTGTGGGCTGCTTCCCACTGA 1238
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841 GGCAGAGGCGCAGAGAGAGGAGTGTGTGTGGGCGATCTTCAAGAGATGAAGTGAAGAGAG 900
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1239 GGCAGAGGCGCAGAGAGAGGAGTGTGTGTGGGCGATCTTCAAGAGATGAAGTGAAGAGAG 1298
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901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
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1299 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1358
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1359 TCAGCTTGAAGGCCCCCGCTGCGAGCAGCAGAGGCTCCCGGCTGTGGCGACCCCTAAGT 1418
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1021 GGCAGAGTCTCTTGGGCGAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
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1419 GGCAGAGTCTCTTGGGCGAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1478
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1081 GGCAGAGTCTCTTGGGCGAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
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1479 GGCAGAGTCTCTTGGGCGAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1538
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1141 GTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
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1201 TGCAGAGTCTCTTGGGCGAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
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1599 TGCAGAGTCTCTTGGGCGAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1658
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1261 CTGAACCTGTATTAATCAACCATCTTCAACAGAGACTTCCGCGCTTCCGAGAGATC 1320
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1659 CTGAACCTGTATTAATCAACCATCTTCAACAGAGACTTCCGCGCTTCCGAGAGATC 1718
|||||
1321 CTGTGCGGCGCGTGAACCAAGAGCGGCTGTGA 1353
|||||
1719 CTGTGCGGCGCGTGAACCAAGAGCGGCTGTGA 1751
|||||

RESULT 8
AA199906
ID AA199906 standard; DNA; 1344 BP.
XX
AC AA199906;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
polymorphic site; allelic variant; cardiovascular disease;
central nervous system disease; adenylyl cyclase; MAP kinase activity;
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KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1344
FT FT /tag= a
FT FT /product= "alpha-2BAR"
FT FT /note= "sequence is deleted for a 9 nucleotide
polymorphic site found at nucleotides 901-909
of the wildtype alpha-2BAR protein (AA199905)"
FT FT
PN WO200179561-A2.
PN
PD 25-OCT-2001.
PD
PF 17-APR-2001; 2001WO-US12575.
PF
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMAL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52118.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
determining whether an individual is at increased risk of developing a
disease associated with the corresponding receptor comprises detecting
a polymorphic site -
XX
PS Claim 5; Page 144-145; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polymorphic site encoding an alpha-2B,
alpha-2A or alpha-2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
of (I), a site comprising cytosine or guanine at position 753 of (II)
or a site comprising (A) (599ggcgggcg) or (B) (ggggcggtgag) at
positions 961-972 of (III). The method may be used for genotyping an
alpha-2B, alpha-2A or alpha-2C receptor gene and further used to determine
whether an individual is at increased risk of developing a disease
associated with alpha-2B, alpha-2A or alpha-2, comprising detecting a
polymorphic site which correlate to disease selected from cardiovascular
disease, central nervous system disease and combinations of these. In
addition, the technique may be used to predict an individual's response
to an alpha-2B, alpha-2A, or alpha-2C agonist (e.g. epinephrine,
norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
rauwolscine, idazoxan, tolazoline, phenoltamine and combinations of
these) by detecting the polymorphic site and correlating the site to a
predetermined response (where the response is correlated to adenylyl
cyclase, MAP kinase activity, phosphorylation or inositol phosphate
levels). The present sequence is that of the third intracellular loop of
the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
polymorphic site found at nucleotides 901-909 of the wildtype gene
(AA199905).
CC
SQ Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;
XX
XX
Query Match 97.9%; Score 1325; DB 23; Length 1344;
Best Local Similarity 99.3%; Pred. No. 36-252;
Matches 1344; Conservative 0; Mismatches 0; Indels 9; Gaps 1;
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QY 61 TTCTCATTTCTTTTACCATCTTGGCAAGCGTCTGTCATCTTGGCTGTGTGACGAGC 120
 DB 61 TTCTCATTTCTTTTACCATCTTGGCAAGCGTCTGTCATCTTGGCTGTGTGACGAGC 120
 QY 121 CGCTGCTGCGGGCCCTTCAGAACCTGTTCCTGTGTGCTGTGCGCGCGCGAGCATCTTG 180
 DB 121 CGCTGCTGCGGGCCCTTCAGAACCTGTTCCTGTGTGCTGTGCGCGCGCGAGCATCTTG 180
 QY 181 GTGGCAGCGCTCATCATCTCTTCTGCTGCGCAACGAGCTGCTGGGCTTACCTGTACTTC 240
 DB 181 GTGGCAGCGCTCATCATCTCTTCTGCTGCGCAACGAGCTGCTGGGCTTACCTGTACTTC 240
 QY 241 CGGCGGACGTGTGCGAGGTGTACCTGGGCGCTGACGAGTCTCTTGTGACCTGTCTATC 300
 DB 241 CGGCGGACGTGTGCGAGGTGTACCTGGGCGCTGACGAGTCTCTTGTGACCTGTCTATC 300
 QY 301 GTGCACTGTGCGCATCATCTGCTGCGCAACCGCTTACTGGGCGGTGAGCGCGCTGAGTAC 360
 DB 301 GTGCACTGTGCGCATCATCTGCTGCGCAACCGCTTACTGGGCGGTGAGCGCGCTGAGTAC 360
 QY 361 AACTCCAGGCGCAACCCCGCGCGCATCATAGTGCATCATCTGTGTGCTCATCTGCGC 420
 DB 361 AACTCCAGGCGCAACCCCGCGCGCATCATAGTGCATCATCTGTGTGCTCATCTGCGC 420
 QY 421 GCGGTCACTGTGCGCGCGCGCTCATCTACAGGCGGCAACGAGGCGCGCGCGCGCGG 480
 DB 421 GCGGTCACTGTGCGCGCGCGCTCATCTACAGGCGGCAACGAGGCGCGCGCGCGCGG 480
 QY 481 CGCCCGCAGTGCAGAGCTCAACGAGAGCGCTGTGATCATCTGCGCTTCAGCATCGATCT 540
 DB 481 CGCCCGCAGTGCAGAGCTCAACGAGAGCGCTGTGATCATCTGCGCTTCAGCATCGATCT 540
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 DB 601 CGCAGCAACCGCAGAGGTCCAGGCGCAAGGCGGCGCTGGGCGAGGTGATCCAGCAG 660
 QY 661 CCGCCGACCGGACCATGTGTGGGCTTGTGCTCAGCCAACTGCCAGCCCTGTGTG 720
 DB 661 CCGCCGACCGGACCATGTGTGGGCTTGTGCTCAGCCAACTGCCAGCCCTGTGTG 720
 QY 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCACTGGGAGGAGGAGGAGGAG 780
 DB 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCACTGGGAGGAGGAGGAGGAG 780
 QY 781 ACCCTGAGAGTCTTGGGACCGGCGCTTGGCCAGCTTGGGCTGCTTCCAACTCA 840
 DB 781 ACCCTGAGAGTCTTGGGACCGGCGCTTGGCCAGCTTGGGCTGCTTCCAACTCA 840
 QY 841 GGCAGGCGCAGAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 891
 DB 841 GGCAGGCGCAGAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 891
 QY 901 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 DB 901 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 QY 961 TCGAGCTTGCAGCGCCCGCTGCGAGCAGGAGCTCCGGGTGCTGGCCACCTCACT 1020
 DB 961 TCGAGCTTGCAGCGCCCGCTGCGAGCAGGAGCTCCGGGTGCTGGCCACCTCACT 1020
 QY 1021 GGCAGGAGTCTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 DB 1021 GGCAGGAGTCTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 QY 1071 GGCAGGAGTCTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1071
 DB 1071 GGCAGGAGTCTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1071
 QY 1081 GGCAGGAGTCTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
 DB 1081 GGCAGGAGTCTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
 QY 1072 GGCAGGAGTCTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1131
 DB 1072 GGCAGGAGTCTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1131
 QY 1141 GTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1200
 DB 1141 GTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1200

DB 1132 GTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1191
 QY 1201 TGCAGAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
 DB 1192 TGCAGAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1251
 QY 1261 CTGAACCTGTGTATCTATCAACCATCTTCAACGAGAGCTTCCGCGCTTCCGAGATC 1320
 DB 1252 CTGAACCTGTGTATCTATCAACCATCTTCAACGAGAGCTTCCGCGCTTCCGAGATC 1311
 QY 1321 CTGTGCGCGCGCGGTGACCCAGACGCGCTGTGTA 1353
 DB 1312 CTGTGCGCGCGCGGTGACCCAGACGCGCTGTGTA 1344
 RESULT 9
 AAD04761
 ID AAD04761 standard; DNA; 1344 BP.
 AC AAD04761;
 DT 04-JUL-2001 (first entry)
 XX
 DE Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
 KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 1..1344
 FT CDS /tag=a
 FT /product="Human alpha2B-adrenoceptor (alpha2B-AR)
 FT /variant protein"
 PN MO200129082-A1.
 PD 26-APR-2001.
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 PF 20-OCT-2000; 2000MO-F100913.
 XX
 PR 22-OCT-1999; 99US-0422985.
 XX
 PA (JUVA-) JUVANTIA PHARMA LTD OY.
 XX
 XX Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
 PI Scheinin M, Salonen JT, Tuominen T, Lakka TA, Nyssönen K;
 PI Salonen R, Kaunonen J, Valkonen V;
 XX
 DR WPI; 2001-300318/31.
 DR P-PSDB; AAE00989.
 XX
 FT New DNA molecule encoding variant specific adrenoceptor protein with
 FT deletion of specific amino acid located in the third intracellular
 FT loop of the polypeptide, for treating vascular contraction of coronary
 FT arteries -
 PS Claim 3; Page 24-26; 37pp; English.
 XX
 CC The present sequence is a gene encoding human alpha2B-adrenoceptor
 CC (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
 CC element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
 CC 18 amino acids (amino acids 294-311), located in the third intracellular
 CC loop of the receptor polypeptide. The variant is obtained by deletion of
 CC three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
 CC gene is located on chromosome 2. Alpha2-AR mediate many of the
 CC physiological effects of the catecholamines, norepinephrine and
 CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating

CC a mammal suffering from vascular contraction of coronary arteries and a
CC disease involving vascular contraction of coronary arteries which is
CC clinically expressed as coronary heart disease (CHD), unstable chronic
CC angina pectoris which is clinically expressed as Prinzmetal's variant
CC form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
CC gene therapy.

Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;

Query Match	97.8%	Score 1323.4	DB 22	Length 1344
PostgreSQL	97.8%	Score 1323.4	DB 22	Length 1344

Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

OY	1	ATGACACACAGAACCCCTACTCCGTGACAGGACACAGCGGCATTAACGGCGGCATACAC	60
Db	1	ATGACACACAGAACCCCTACTCCGTGACAGGACACAGCGGCATTAACGGCGGCATACAC	60
OY	61	TTCTCATATCTTTTAACATCTTGGGCAACGCTCTGTCATCTGGCTGTGTGACCAAGC	120
Db	61	TTCTCATATCTTTTAACATCTTGGGCAACGCTCTGTCATCTGGCTGTGTGACCAAGC	120
OY	121	GCGTCGCTGCGGCGCCCTCAGAAACCTGTACTGTGATCGCTGGCCGCGCGGCATACCTTG	180
Db	121	GCGTCGCTGCGGCGCCCTCAGAAACCTGTACTGTGATCGCTGGCCGCGCGGCATACCTTG	180
OY	181	GTGGCCACGCTCATATCCCTTTCTTGCTGCTGGCCAAAGACTGCTGGAAGCTTAATGTTTTC	240
Db	181	GTGGCCACGCTCATATCCCTTTCTTGCTGCTGGCCAAAGACTGCTGGAAGCTTAATGTTTTC	240
OY	241	CGGCGCACGTGGTGGGAGGTGTAACTGCGGGCTTGACAGTGTCTTCTTGACACTGTGTCAATC	300
Db	241	CGGCGCACGTGGTGGGAGGTGTAACTGCGGGCTTGACAGTGTGTCTTCTTGACACTGTGTCAATC	300
OY	301	GTGCACCTGTGGGCATCAGCCTGGAACCGCTACTGCGGCGGTGAGCGCGCGCTGAGAGTAC	360
Db	301	GTGCACCTGTGGGCATCAGCCTGGAACCGCTACTGCGGCGGTGAGCGCGCGCTGAGAGTAC	360
OY	361	AACTCCAAAGCGCAACCCCGCGCGGCATCAAGTGATCATCTCTCACTGTGTGCTCATTCGCC	420
Db	361	AACTCCAAAGCGCAACCCCGCGCGGCATCAAGTGATCATCTCTCACTGTGTGCTCATTCGCC	420
OY	421	GCGCTCATCTGCTGCGCGCGCCCTCATCTTCAAGGGGGAGACAAAGGGCCCCAGCGCGCGGG	480
Db	421	GCGCTCATCTGCTGCGCGCGCCCTCATCTTCAAGGGGGAGACAAAGGGCCCCAGCGCGGG	480
OY	481	CGCCCCCAGTGCAGCTCAACCAAGAGAGGCTGGTACATCTTGACTTCAGACATCGATCT	540
Db	481	CGCCCCCAGTGCAGCTCAACCAAGAGAGGCTGGTACATCTTGACTTCAGACATCGATCT	540
OY	541	TTCTTTTGCTCTTGCTGCTCATATGATCTTGTGTACTCTGCGCATCTTACTGATTCGCCAAA	600
Db	541	TTCTTTTGCTCTTGCTGCTCATATGATCTTGTGTACTCTGCGCATCTTACTGATTCGCCAAA	600
OY	601	CGACGCAACCGCAGAGAGTCCACAGGGCCAAAGGGGGGCTGGGCAAGGATGATCCAGACAG	660
Db	601	CGACGCAACCGCAGAGAGTCCACAGGGCCAAAGGGGGGCTGGGCAAGGATGATCCAGACAG	660
OY	661	CCCCGACCCGACCATGTGTGGGGCTTTTGAGCTTAGCCAAACTGCGACGCTCTGCTGTG	720
Db	661	CCCCGACCCGACCATGTGTGGGGCTTTTGAGCTTAGCCAAACTGCGACGCTCTGCTGTG	720
OY	721	GCTTGTGCGAGAGGTCAACGGACACTGGAAGTCCACTGGGGAGAAAGAGAGGGGGAG	780
Db	721	GCTTGTGCGAGAGGTCAACGGACACTGGAAGTCCACTGGGGAGAAAGAGAGGGGGAG	780
OY	781	AACCTCGAAGATCTGGGACCCGAGGCTTGGCCACCCAGTTGGGGCTGCGCTTCCCACTCA	840
Db	781	AACCTCGAAGATCTGGGACCCGAGGCTTGGCCACCCAGTTGGGGCTGCGCTTCCCACTCA	840
OY	841	GCGCCAGGGCCAGAGAGAGGTGTTTGTGGGGCATCTTCAGAGATTAAGCTGAAGAGAG	900
Db	841	GCGCCAGGGCCAGAGAGAGGTGTTTGTGGGGCATCTTCAGAGATTAAGCTGAAGAGAG	900

[illegible]

RESULT 10

ID AAD44388 standard; DNA; 1344 BP.

AC AAD44388;

DT 13-DEC-2002 (first entry)

DE Human alpha-2B-adrenoceptor variant DNA.

KW Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;

XX

OS Synthetic.

FH	Key	Location/Qualifiers
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99	99	99
100	100	100

FT / *tag= a

FT protein^a

PN WO200266617-A1.

PD 29-AUG-2002.

PF 13-FEB-2002; 2002WO-FI00113.

PR 20-FEB-2001; 2001FI-0000323.

PA (JURI-) JURILAB LTD OY

PI Salonen J;

DR WPI; 2002-667063/71.

XX

PT by determining the pattern of alleles encoding a variant

PT alpha-2-adrenoceptor -

XX Disclosure: Page 24-26; 35pp; English.

PS The invention relates to a method for detecting a risk of hypertension

CC by determining the pattern of alleles encoding a variant alpha-2B-

CC adrenoreceptor (AK) protein. The methods and compositions of the invention

CC are useful for detecting risks and targeting treatment for hypertension.

CC The kit is also useful for selecting for clinical drug trials testing

CC the antihypertensive effect of compounds. The present sequence is human

CC alpha-2B-adrenoreceptor variant DNA.

XX Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;

XX

Query Match 97.8%; Score 1323.4; DB 24; Length 1344;

Best Local Similarity 99.3%; Pred. No. 6.3e-252;

Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

1 ATGAGCAGCAGGAGCCCTACTCCGTCAGAGCCACAGCGGCCCATAGCGGCGCATCAC 60

1 ATGAGCAGCAGGAGCCCTACTCCGTCAGAGCCACAGCGGCCCATAGCGGCGCATCAC 60

61 TTCTCATCTCTTACCATCTTGGCAGAGCTCTGTGATCTCTGGCTGTGACACAGC 120

61 TTCTCATCTCTTACCATCTTGGCAGAGCTCTGTGATCTCTGGCTGTGACACAGC 120

61 TTCTCATCTCTTACCATCTTGGCAGAGCTCTGTGATCTCTGGCTGTGACACAGC 120

121 CGCTGCTGGCGGCGCCCTCAGAGACCTGTCTGGTGTCTGGCGCGCCGCAATCTTG 180

121 CGCTGCTGGCGGCGCCCTCAGAGACCTGTCTGGTGTCTGGCGCGCCGCAATCTTG 180

121 CGCTGCTGGCGGCGCCCTCAGAGACCTGTCTGGTGTCTGGCGCGCCGCAATCTTG 180

181 GTGGCAGCTCATCATCTCTTCTCGTGGCCACAGAGCTGTGGGTCTAGTACTTC 240

181 GTGGCAGCTCATCATCTCTTCTCGTGGCCACAGAGCTGTGGGTCTAGTACTTC 240

181 GTGGCAGCTCATCATCTCTTCTCGTGGCCACAGAGCTGTGGGTCTAGTACTTC 240

241 CGGCGCAGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300

241 CGGCGCAGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300

241 CGGCGCAGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300

301 GTGACAGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 360

301 GTGACAGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 360

301 GTGACAGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 360

361 AACTCCAGCGCAGCCCGCGCGCATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420

361 AACTCCAGCGCAGCCCGCGCGCATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420

361 AACTCCAGCGCAGCCCGCGCGCATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420

421 GCGGTATCTCGCTGCGCGCCCTCATCTCAAGAGGCGACAGAGGCGCCCGCGCGG 480

421 GCGGTATCTCGCTGCGCGCCCTCATCTCAAGAGGCGACAGAGGCGCCCGCGCGG 480

421 GCGGTATCTCGCTGCGCGCCCTCATCTCAAGAGGCGACAGAGGCGCCCGCGCGG 480

481 CGGCGCAGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540

481 CGGCGCAGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540

481 CGGCGCAGTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540

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541 TTCTTGTCTCTTGTCTCATCATCATCATCATCATCATCATCATCATCATCATCAT 600

541 TTCTTGTCTCTTGTCTCATCATCATCATCATCATCATCATCATCATCATCATCAT 600

601 CGCAGCAACCGCAGAGTCCAGAGGCGCAAGAGGCGCGCTGGAGAGTGAAGTGA 660

601 CGCAGCAACCGCAGAGTCCAGAGGCGCAAGAGGCGCGCTGGAGAGTGAAGTGA 660

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661 CGCAGCAACCGCAGAGTCCAGAGGCGCAAGAGGCGCGCTGGAGAGTGAAGTGA 720

661 CGCAGCAACCGCAGAGTCCAGAGGCGCAAGAGGCGCGCTGGAGAGTGAAGTGA 720

661 CGCAGCAACCGCAGAGTCCAGAGGCGCAAGAGGCGCGCTGGAGAGTGAAGTGA 720

721 GCTTCTGCGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780

721 GCTTCTGCGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780

721 GCTTCTGCGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780

781 ACCCTGAAAGTATCTGGAGCCCGGCGCTTGGCAGCCAGTGGGCTGCTTCCCACTCA 840

781 ACCCTGAAAGTATCTGGAGCCCGGCGCTTGGCAGCCAGTGGGCTGCTTCCCACTCA 840

781 ACCCTGAAAGTATCTGGAGCCCGGCGCTTGGCAGCCAGTGGGCTGCTTCCCACTCA 840

QY 841 GGCAGGGCCAGAGAGAGGAGGTTTGTGGGATCTCTCAGAGATGAAGCTGAAGAGAG 900

DB 841 GGCAGGGCCAGAGAGAGGAGGTTTGTGGGATCTCTCAGAGATGAAGCTGAAGAGAG 900

QY 901 GAAG 960

DB 901 GAAG 960

QY 901 GAAG 960

DB 901 GAAG 960

QY 961 TGAAGTGAAG 1020

DB 961 TGAAGTGAAG 1020

QY 961 TGAAGTGAAG 1020

DB 961 TGAAGTGAAG 1020

QY 1021 GGCAGAGTCTCTCTGAG 1080

DB 1021 GGCAGAGTCTCTCTGAG 1080

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DB 1021 GGCAGAGTCTCTCTGAG 1080

QY 1081 GGCAGAGTCTCTCTGAG 1140

DB 1081 GGCAGAGTCTCTCTGAG 1140

QY 1081 GGCAGAGTCTCTCTGAG 1140

DB 1081 GGCAGAGTCTCTCTGAG 1140

QY 1072 GGCAGAGTCTCTCTGAG 1131

DB 1072 GGCAGAGTCTCTCTGAG 1131

QY 1141 GGCAGAGTCTCTCTGAG 1200

DB 1141 GGCAGAGTCTCTCTGAG 1200

QY 1132 GGCAGAGTCTCTCTGAG 1191

DB 1132 GGCAGAGTCTCTCTGAG 1191

QY 1201 TGAAGAGTCCCATGAG 1260

DB 1201 TGAAGAGTCCCATGAG 1260

QY 1192 TGAAGAGTCCCATGAG 1251

DB 1192 TGAAGAGTCCCATGAG 1251

QY 1261 CTGAAGCTCTGTTATCTACCATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1320

DB 1261 CTGAAGCTCTGTTATCTACCATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1320

QY 1252 CTGAAGCTCTGTTATCTACCATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1311

DB 1252 CTGAAGCTCTGTTATCTACCATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1311

QY 1321 CTGTCGCGCCCGTGAG 1353

DB 1321 CTGTCGCGCCCGTGAG 1353

QY 1312 CTGTCGCGCCCGTGAG 1344

DB 1312 CTGTCGCGCCCGTGAG 1344

RESULT 11

ABL32075/c

ID ABL32075 strand; DNA; 6904 BP.

AC ABL32075;

DT 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 48.

XX Human: immune system disease; cytosine methylation; antiasthmatic;

XX antiarteriosclerotic; antiamebic; cytosolic; neocytotic;

XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

XX antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;

XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

XX gene; ds.

XX Homo sapiens.

OS WO200200928-A2.

PN 03-JAN-2002.

PD 02-JUL-2001; 2001WO-EP07537.

PF 30-JUN-2000; 2000DB-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIDEMIOLOGICS AG.

XX Olek A. Pfenbrock C. Berlin K;

XX WPI; 2002-130909/17.


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QY 241 CGGCGACGCTGGTGCAGAGGTGTAAGTGGGCTGCGACGTGCTCTTTCGACCTTCGTCATC 300
DB 5241 CGGCGTACGCTGGTGCAGAGGTGTAAGTGGGCTGCGACGTGCTCTTTCGATTCGTTATTC 5300
QY 301 GTGCACTGTGGCCGCTACGACCGCTACCTGGGCGGTGAGCCGCGCTGAGGTAC 360
DB 5301 GTGATTTTGTGCTTATGTTAGTTGAGTCTTATTTGGGTGAGTGGCGGTTGAGGTAT 5360
QY 361 AACTCCAGCGCACCCCGCGCATCAAGTGCATCATCTCTGCTGAGTGCATCGCC 420
DB 5361 AATTTTAAACGTAATTTCCGCGGTATTAAGTGTATTTATTTATGTGTGTTATTCGTC 5420
QY 421 GCCGTCATCTGCTGCGCCCTCATCTCAAGAGGCGACAGGCGCCCAAGCCGCGCGG 480
DB 5421 GTTCGTTATTTGCTGTGCTGTTTATTTATTAAGGCGGATTAAGGCTTTTATAGTGGCGG 5480
QY 481 CGCCCGCATGTCAAGCTCAACGAGAGGCTGTATCATCTGCGCTCCAGCATCGATCT 540
DB 5481 CGTTTATGTAAGTTATTAATTAAGAGGTTGGTATATTTGTTTATGTAATCGGATTT 5540
QY 541 TTCTTGTCTCTTGCCTCATCATGATCTGTCTACCTGGGATCTTACCGTATCGCCAA 600
DB 5541 TTTTGTGTTTGTGTTTATTTATGATTTTGTGTTATTTGCGTATTTATTTGATCGTTAA 5600
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DB 5601 CGTAGTATCGTAGAGGTTTATAGGCTTAAAGGCGGCTTTGGTAAAGGTGATTAAGTAA 5660
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DB 5841 GGTGAGGCTTAAAGAGAGGCTTTGTGGGCTATTTTATAGAGATGAAGTT----- 5891
QY 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 5892 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5951
QY 961 TCAGCTTGCAGGCGCCCGCTGCAGCAGCAGAGGCTCCCGG 1003
DB 5952 TTAGTTTGTAGTTTTCGTTGTGTAAGTATTAAGGCTTTCCGG 5994
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RESULT 14
AAD28364
AAD28364 standard; DNA; 6904 BP.
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AC AAD28364;
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DT 22-APR-2002 (first entry)
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DE Human chemically treated genomic DNA #5.
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Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
behavioral disorder; neurological; psychiatric; cancer; schizophrenia;
Tourette's syndrome; smoking; human immunodeficiency virus dementia;
drug abuse; migraine; de.
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OS Homo sapiens.
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XX WO200202809-A2.
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XX
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PD 10-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07540.
PF
XX 30-JUN-2000; 2000DE-1032529.
PR
XX 01-SEP-2000; 2000DE-1043826.
PA (EPIS-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-154759/20.
DR
XX
XX Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -
XX
XX Claim 1; Page 40-44; 190pp; English.
XX
CC The invention relates to nucleic acid comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviour in schizophrenic
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
SQ Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 1 other;
XX
Query Match 37.9%; Score 512.6; DB 24; Length 6904;
Best Local Similarity 70.3%; Pred. No. 7,5e-92;
Matches 705; Conservative 0; Mismatches 289; Indels 9; Gaps 1;
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DB 5001 ATGATATTATTAAGATTTTATTTATTCGTAAGTAAAGCGTTATTAAGCGGATTAAT 5060
QY 61 TTCCTATCTCTTTACCATCTTCGCAACGCTGTGTATCTGCTGTGTGACAC 120
DB 5061 TTTTATTTTATTTTATTAATTTTCGTAACGTTTGTGTATTTTGTGTGATTAAT 5120
QY 121 CGCTGCTGCGGCGCCCTCAGAACCTGTCTGTGTGTGCTGCGCGCGCGCATCTTG 180
DB 5121 CGTTGCTGCGGCTTTTATTAAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5180
QY 181 GTGGCAGCGCTCATCATCCCTTTCTGCTGCGCAAGAGCTGTGGCTACTGTACTTC 240
DB 5181 GTGGTTAGCTTATTAATTTTTCGTTGTTAAGAGATGTGGGTTATGATTTT 5240
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DB 5241 CGGCGTACGCTGTGCGAGGTGTATTTGGGCTGCAAGTCTTTTGTATTTGTTATTC 5300
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DB 5301 GTGATTTTGTGCTTATTAATTTGAGATCTTATTTGGGTGAGTGGCGGTTGAGGTAT 5360
QY 361 AACTCCAGCGCACCCCGCGCATCAAGTGCATCATCTCTGCTGAGTGCATCGCC 420
DB 5361 AATTTTAAACGTAATTTCCGCGGTATTAAGTGTATTTATTTATGTGTGTTATTCGTC 5420
QY 421 GCCGTCATCTGCTGCGCCCTCATCTCAAGAGGCGACAGGCGCCCAAGCCGCGCGG 480
DB 5421 GTTCGTTATTTGCTGTGCTGTTTATTTATTAAGGCGGATTAAGGCTTTTATAGTGGCGG 5480
QY 481 CGCCCGCATGTCAAGCTCAACGAGAGGCTGTATCATCTGCGCTCCAGCATCGATCT 540
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DB 550 TTCCCGCCGCTGCTCT---CGCTTACCCGCCAGCCCGACGCGCGCCCTTACCCGCGAGTGC 606
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DB 607 GGCCTTCAAGACGAGACTGTGTACATCTGTCTCTGTGATGAGCTCTTCTTTCGCGCC 666
QY 553 TGCCTCATCATGATCTTGTCTTACCTGCGCATCTTACCTGTATGCGCAACGACGACCGC 612
DB 667 TGCCTCATCATGAGCTGTGTCTACGCGCGCATCTTACGAGTGGCCAAAGCGTCCGACGCG 726
QY 613 AGAGGTCCAGGAGCCAAAGGAGGCGCTGAGCGAGGTGAGTCCAAAGCAGCCCGACCGAC 672
DB 727 A-----CGCTCAGGAGAAAGCGCGCCCGGTGAGCGCCGACGATGCGTCCCGAC 776
QY 673 CATGTGAGGCGCTTTGCGCTCAAGCCAACTGCGAGCCCTGAGCTCTGTGCTTCTGCGAGA 732
DB 777 TACCG-----AAAAAGGCTGAGGCGCGCGCGAGCGAGCGAGAAC 818
QY 733 GAGGTCAACGAGCACTCGAAGTCACTGAGGAGAAAGAGAGGAGGAGAGCCCTGAAGAT 792
DB 819 GGGCACTGAGCGCGCCCGCGCGCGCGAGCTGAGCCGAGCAGAGCAGCGCGCGCGAG 878
QY 793 ACTGAGACCCGAGGCTTGTGCACCCAGTTGAGGCTGCCCTTCCAACTCAGGCGAGGCGCAG 852
DB 879 AGGCGG-----CGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 903
QY 853 AAGGAGGCTGTGTTGTGAGGCGATCTCGAGAGATGAAGCTGAAGAGAGAGAGAGAG 912
DB 904 CGGAGCGGCGCGCGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 963
QY 913 GAGGAGAGAGAGAGAGTGAACCCGAGGAGTGCAGTGTCTCCGAGCTCAGCTTGCAGC 972
DB 964 GCGGAGCGCGGAGCGGAGTGAAGTGGGAGCGCTGACCGCTTCAAGTCTCCGAGGCGCGGT 1023
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DB 1024 GGCCTGCTTCCGCGCGCGAGCTGCGGCTCGTGAAGTCTTCTGTGCGCGCGCGCGG 1083
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DB 1084 GCGCGCAGCAGCGT-----GTGCGCGCGCAAGGTGCGCGCAGCGG 1122
QY 1093 CGGAGAGAGCGCTTCACTTGTGCTGAGCTGTGATTTGAGGCTTTTGTGCTGTGCG 1152
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QY 1213 CATGAGCTTTCAGTGTCTTCTTGTGATGCGCTACTGCAACAGCTCACTGAACCTGTT 1272
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QY 1273 ATCTACACCATTTGAACAGAGACTTCCCGCTTCCGAGAGATCTGTGCGCGCG 1332
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QY 1333 TGA 1336
DB 1363 AGA 1366

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Job time : 404.318 secs

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 20:26:52 ; Search time 89.7987 Seconds
(without alignments)
6650.337 Million cell updates/sec

Title: US-09-692-077D-1

Perfect score: 1353

Sequence: 1 atgacacacagaccacca.....ggaccacagcgcgcgcga 1353

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents NA:*

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6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1349.8	99.8	2072	4 US-09-016-434-1181	Sequence 1181, Ap
2	430	32.8	1382	4 US-09-016-434-1256	Sequence 1256, Ap
3	430	31.8	3604	4 US-09-016-434-1180	Sequence 1180, Ap
4	184.8	13.7	3335	1 US-07-676-174A-1	Sequence 1, Appl
5	163.4	12.1	3335	1 US-08-194-338-1	Sequence 1, Appl
6	158.6	11.7	921	1 US-08-722-001-17	Sequence 17, Appl
7	158.6	11.7	1567	1 US-08-722-001-24	Sequence 24, Appl
8	157	11.6	1738	1 US-08-334-698-3	Sequence 3, Appl
9	157	11.6	1738	1 US-08-228-932-3	Sequence 3, Appl
10	157	11.6	1738	1 US-08-468-939-3	Sequence 3, Appl
11	157	11.6	1738	2 US-08-406-855A-3	Sequence 3, Appl
12	157	11.6	1738	2 US-08-722-001-3	Sequence 3, Appl
13	157	11.6	1738	2 US-08-244-354-3	Sequence 3, Appl
14	157	11.6	1738	3 US-09-206-899-3	Sequence 3, Appl
15	157	11.6	1738	4 US-09-444-783-3	Sequence 3, Appl
16	157	11.6	1738	4 US-09-688-415-3	Sequence 3, Appl
17	157	11.6	1738	4 US-09-016-434-11402	Sequence 1402, Ap
18	157	11.6	1738	5 PCT-US95-04203-3	Sequence 1402, Ap
19	149.6	11.1	1621	1 US-08-722-001-13	Sequence 13, Appl
20	149.6	11.1	1776	1 US-08-722-001-29	Sequence 29, Appl
21	149.6	11.1	2002	4 US-09-016-434-11172	Sequence 1172, Ap
22	149.6	11.1	2140	1 US-08-334-698-1	Sequence 1, Appl
23	149.6	11.1	2140	1 US-08-228-932-1	Sequence 1, Appl
24	149.6	11.1	2140	1 US-08-468-939-1	Sequence 1, Appl
25	149.6	11.1	2140	2 US-08-406-855A-1	Sequence 1, Appl
26	149.6	11.1	2140	2 US-08-722-190-1	Sequence 1, Appl
27	149.6	11.1	2140	3 US-08-244-354-1	Sequence 1, Appl

28	149.6	11.1	2140	3 US-09-206-899-1	Sequence 1, Appl
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31	149.6	11.1	2140	5 PCT-US95-04203-1	Sequence 1, Appl
32	139.8	10.3	1601	1 US-08-722-001-7	Sequence 7, Appl
33	139.8	10.3	1997	1 US-08-722-001-27	Sequence 27, Appl
34	139.8	10.3	2004	1 US-08-722-001-11	Sequence 11, Appl
35	138.4	10.2	1930	4 US-09-016-434-1171	Sequence 1171, Ap
36	138.4	10.2	2463	1 US-08-370-542-1	Sequence 1, Appl
37	138.4	10.2	2463	1 US-08-542-358-1	Sequence 1, Appl
38	138.4	10.2	2463	3 US-09-018-351-1	Sequence 1, Appl
39	138.2	10.2	1639	1 US-08-334-698-5	Sequence 5, Appl
40	138.2	10.2	1639	1 US-08-228-932-5	Sequence 5, Appl
41	138.2	10.2	1639	1 US-08-468-939-5	Sequence 5, Appl
42	138.2	10.2	1639	2 US-08-406-855A-5	Sequence 5, Appl
43	138.2	10.2	1639	2 US-08-722-190-5	Sequence 5, Appl
44	138.2	10.2	1639	3 US-08-244-354-5	Sequence 5, Appl
45	138.2	10.2	1639	3 US-09-206-899-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-016-434-1181
; Sequence 1181, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9178197
; US-09-016-434-1181
Query Match 99.8%; Score 1349.8; DB 4; Length 2072;
Best Local Similarity 99.9%; Pred. No. 1.6e-252;

Mon Feb 9 08:28:39 2004

us-09-692-077d-1.in1

Page 2

Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGACACACAGAGACCCCTTACCTGCTGAGAGGCGACAGCGGCATAGCGGCGCATCAC 60
DB 413 ATGAGACACACAGAGACCCCTTACCTGCTGAGAGGCGACAGCGGCATAGCGGCGCATCAC 472
QY 61 TTCTCATTTCTTTTACATCTTTCGCAACGCTGTGATCTTCGCTGTGTTGACACAC 120
DB 473 TTCTCATTTCTTTTACATCTTTCGCAACGCTGTGATCTTCGCTGTGTTGACACAC 532
QY 121 CGCTGCTGCGCGCCCTCAGAACCTGTTCGTGTGCTGTGCGCGCGCGCGCATCTG 180
DB 533 CGCTGCTGCGCGCCCTCAGAACCTGTTCGTGTGCTGTGCGCGCGCGCGCATCTG 552
QY 181 GTGCGACAGGTCATCATCTCTTCTGCTGCGCAAGAGCTGTGAGGCTACTGTACTTC 240
DB 593 GTGCGACAGGTCATCATCTCTTCTGCTGCGCAAGAGCTGTGAGGCTACTGTACTTC 652
QY 241 CGGCGACAGTGTGAGGTCATCTGCGCGCTGAGCGCTGTCTTCTGCACTTCTGCACTC 300
DB 653 CGGCGACAGTGTGAGGTCATCTGCGCGCTGAGCGCTGTCTTCTGCACTTCTGCACTC 712
QY 301 GTGCGACAGTGTGAGGTCATCTGCGCGCTGAGCGCTGTCTTCTGCACTTCTGCACTC 360
DB 713 GTGCGACAGTGTGAGGTCATCTGCGCGCTGAGCGCTGTCTTCTGCACTTCTGCACTC 772
QY 361 AACTCCAGGCGACCCCGCGCGCGCATCAAGTCATCTCTGCTGTGAGGCTACTGTACTTC 420
DB 773 AACTCCAGGCGACCCCGCGCGCGCATCAAGTCATCTCTGCTGTGAGGCTACTGTACTTC 832
QY 421 GCGCTCATCTGCTGCGCGCGCTCTCATCTCAAGGCGCGACAGAGCGCGCGCGCGCG 480
DB 833 GCGCTCATCTGCTGCGCGCGCTCTCATCTCAAGGCGCGACAGAGCGCGCGCGCGCG 892
QY 481 GCG 540
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DB 1073 CGGAGAACCGGAGAGGTCCTCAGGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCG 1132
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DB 1193 ACCCTGTAAGTATCTGAGAGCCCGGCTTTCAGCAAGGTCGCTGCTTCCCACTCA 1252
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QY 901 GAG 960
DB 1313 GAG 1372
QY 961 TCAGCTTGAAGCCCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1432
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DB 1433 GCGCGAGGTCCTGCG 1492

QY 1081 GCGAGCTGACCCCGGAGAGAGCGCTTCACTTGTGCTGCTGCTGCTGCTGCTT 1140
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QY 1261 CTGAGACCTGTATCTACACATCTTCAACAGAGCTTCCGCGCGCTTCCGAGAGATC 1320
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QY 1321 CTGAGCGCGCGTGAACCCAGAGAGCGCGCTGCTGA 1353
DB 1733 CTGAGCGCGCGTGAACCCAGAGAGCGCGCTGCTGA 1765

RESULT 2
US-09-016-434-1256
Sequence 1256, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Jeffrey A. Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1256:
SEQUENCE CHARACTERISTICS:
LENGTH: 1382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g219405
US-09-016-434-1256
Query Match 32.8%; Score 444; DB 4; Length 1382;
Best Local Similarity 62.2%; Pred. No. 1.7e-77;
Matches 823; Conservative 0; Mismatches 405; Indels 96; Gaps 4;

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Qy 13 GACCCCTACTCCGTGAGGCCACAGCGCCATAGCCGCGGCATCATCTTCTCTATCTC 72
Db 132 GGGCAGTACTCGGCGGGGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 191
Qy 73 TTTTACCATTTTGGGCAAGCCTCTGATCTGAGCTGTGTGAACAGCCGCTGCTGCGC 132
Db 192 TTACCGTGTGTGGCAAGCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 251
Qy 133 GGGCCCTCAGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 192
Db 252 GGGCCACAGAACCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 311
Qy 193 ATCATCTCTTCTGCTGAGCCCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 252
Db 312 GTCATGTCTTCTGCTGAGCCCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 371
Qy 253 TGCAGAGTGTACCTGTGCGCTGCAAGCTGTCTTCTGTGCACTGTGTGTGTGTGTGTGT 312
Db 372 TGCAGAGTGTACCTGTGCGCTGCAAGCTGTCTTCTGTGCACTGTGTGTGTGTGTGTGT 431
Qy 313 GGCATCAGCTGTGACCGCTACCTGTGAGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGT 372
Db 432 GGCATCAGCTGTGAGCGCTACCTGTGAGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGT 491
Qy 373 ACCCGCGCGCGCATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 432
Db 492 ACACACGCGCGCGCATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
Qy 433 CTGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 492
Db 552 TTCCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 608
Qy 493 AAGCTCAACAGAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 552
Db 609 GGCCTCAACAGAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 668
Qy 553 TGCCTCATCATGTATCTTGTCTACCTGTGCGCATCTGTGTGTGTGTGTGTGTGTGTGT 612
Db 669 TGCCTCATCATGTATCTTGTCTACCTGTGCGCATCTGTGTGTGTGTGTGTGTGTGTGT 728
Qy 613 AGAGGTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 672
Db 729 A-----CGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 761
Qy 673 CATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 732
Db 762 GACGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 821
Qy 733 GAGGTCAACGAGACCTCGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 792
Db 822 GGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 881
Qy 733 ACTGGGACCCGGGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 852
Db 882 AGGCGGCGGC-----GCGGCGGCGGC 902
Qy 853 AAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 912
Db 903 TTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 962
Qy 913 GAGGAGGAGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 972
Db 963 CAGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1022
Qy 973 CCCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1032
Db 1023 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1082
Qy 1033 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1092
Db 1083 AGCAGC-----GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1115

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Qy 1093 CGGAGAGAGCGCTTCAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1152
Db 1116 CGGAGAGAGCGCTTCAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1175
Qy 1153 TTTCCCTTCTTCTTCAAGCTACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1212
Db 1176 TTCCCTTCTTCTTCAAGCTACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1235
Qy 1213 CATGGCTCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1272
Db 1236 GGGCGGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1295
Qy 1273 ATCTACACCATCTTCAACGAGACTTCCGCGCTTCCGAGAGATCTGTGTGTGTGTGT 1332
Db 1296 ATCTACAGGCTTCAACGAGATTTCCGCGGATCTTCAACGATCTCTTCCGAGCG 1355
Qy 1333 TGGG 1336
Db 1356 AGGA 1359

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RESULT 3
US-09-016-434-1180
; Sequence 1180, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3604 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9178195
; US-09-016-434-1180
Query Match 31.8%; Score 430; DB 4; Length 3604;
Best Local Similarity 61.7%; Pred. No. 9,9e-75;
Matches 832; Conservative 0; Mismatches 435; Indels 81; Gaps 6;

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15 CCCCTACTCCGTCAGGCGCAGCCGCGCATAGCGGCGCCATCACCTTCCTCATCTCTT 74
DB CCCCTACTCCGTCAGGCGCAGCCGCGCATAGCGGCGCCATCACCTTCCTCATCTCTT 2214
QY 75 TACATCTTCCGTCAGGCGCAGCCGCGCATAGCGGCGCCATCACCTTCCTCATCTCTT 134
DB 2215 CACCGTGTCCGTCAGGCGCAGCCGCGCATAGCGGCGCCATCACCTTCCTCATCTCTT 2274
QY 135 CCGTCAGAACCTGTCTCTGCGTGTCTGCGCGCGCGCGCATAGCGGCGCCATCACCTTCCT 194
DB 2275 GCGCCCAAAACCTGTCTCTGCGTGTCTGCGCGCGCGCGCATAGCGGCGCCATCACCTTCCT 2334
QY 195 CATCCCTTCTGCTGCGCGCGCATAGCGGCGCCATCACCTTCCTGATCTTCGCGCGCGCGCG 254
DB 2335 CATCCCTTCTGCTGCGCGCGCATAGCGGCGCCATCACCTTCCTGATCTTCGCGCGCGCGCG 2394
QY 255 CGAGTGTACTGCGCGCGCATAGCGGCGCCATCACCTTCCTGATCTTCGCGCGCGCGCGCG 314
DB 2395 CGAGTGTACTGCGCGCGCATAGCGGCGCCATCACCTTCCTGATCTTCGCGCGCGCGCGCG 2454
QY 315 CATAGCTGTGAGCCGCTACTGCGCGCGCATAGCGGCGCCATCACCTTCCTGATCTTCGCGCG 374
DB 2455 CATAGCTGTGAGCCGCTACTGCGCGCGCATAGCGGCGCCATCACCTTCCTGATCTTCGCGCG 2514
QY 375 CCGCGCGCGCGCATAGCGGCGCCATCACCTTCCTGATCTTCGCGCGCGCGCGCGCGCGCG 434
DB 2515 GCGCGCGCGCGCATAGCGGCGCCATCACCTTCCTGATCTTCGCGCGCGCGCGCGCGCGCG 2574
QY 435 GCG 485
DB 2575 CCG 2634
QY 486 CCACTGTCACTCAACAGAGCG 545
DB 2635 GCGCTGTGAGATCAACAGAGCG 2694
QY 546 TGCTCTTGTGCTCATCATCTTCCTGATCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 605
DB 2695 GCGCTCTTGTGCTCATCATCTTCCTGATCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2754
QY 606 CAACCGCAGAGGTCG 665
DB 2755 CAACCGCAGAGGTCG 2795
QY 666 ACCCGCAGATGT 725
DB 2796 CCG 2836
QY 726 TGCGAGAGAGGTCAACAGAGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 785
DB 2837 GCG 2889
QY 786 TGAAGATCTGTGAGCCG 845
DB 2890 CCACTCAACCG 2949
QY 846 GCGCGCAGAGAGGTCG 905
DB 2950 GGAACCTGTGAGAGGTCG 3009
QY 906 GGAAG 965
DB 3010 CGAGCGCGGTCTCCCG 3064
QY 966 TTGAGCG 1025
DB 3065 GCG 3119
QY 1026 GCGTGTCTCTGTGAG 1085
DB 3120 GCGCGCGAG 3171
QY 1086 GGTAGCCCGGAG 1145

DB 3172 GCAAGACCGCAG 3231
QY 1146 CCGT 1205
DB 3232 GTGCTGT 3282
QY 1206 GGTGCG 1265
DB 3283 CGTGTGAG 3342
QY 1266 CCGT 1325
DB 3343 CCGGT 3402
QY 1326 CCG 1385
DB 3403 TCG 3460

RESULT 4

US-07-676-174A-1

Sequence 1, Application US/07676174A

Patent No. 5344776

GENERAL INFORMATION:

APPLICANT: Vantor, J. Craig

TITLE OF INVENTION: Octopamine receptor

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN, DABRY & CUSHMAN

STREET: Eleventh Floor, 1615 L. Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036-5601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/676,174A

FILING DATE: 19910328

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Scott, Watson T.

REGISTRATION NUMBER: 26,581

REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000

TELEFAX: (202) 861-8944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3335 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 319..2121

US-07-676-174A-1

Query Match

Best Local Similarity

Matches 351; Conservative

Score 184.8; DB 1;

Pred. No. 2.4e-27;

Indels 0; Gaps 0;

Mismatches 277;

2 TGAACACACAG 61

611 TGAACACACAG 670

62 TGAACACACAG 121

Db 671 TCATTATCTGCTGACATCATCGGAGACATCTGATGTTCTGATGTTTCACTTACA 730
 Qy 122 GCTGCTGCGCGCCCTCAGAACCTGTTCTGTTGCTGCTGCGCGCGGACATCTTGG 181
 Db 731 AGCCGCTGGGACATGTCAGAACTTTTCACTGATGCTGCGGCGGACATCTTACA 790
 Qy 182 TGGCCACGCTCATCTCTTTCTGCTGCGCAACGAGCTGCTGAGCTACTGTTACTTCC 241
 Db 791 TGGCCCTTGGGCTGCGCTTCAAGTGGCTTACTGATCTGCGGCGGCTGGAGTTGG 850
 Qy 242 GGGCAGCTGCTGCGGAGTGTACTGCTGCGCTGAGCTGCTTCTGCACTCTGCTCATG 301
 Db 851 GCATCAGCTGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 910
 Qy 302 TGCACCTGCTGCGCATCAGCTGCTGAGCGGCTGCTGAGCGCGGCTGAGTACA 361
 Db 911 TGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 970
 Qy 362 ACTCCAGCGCACCCCGCGCGCGCATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCT 421
 Db 971 CCCAGAGAGAGACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1030
 Qy 422 CCGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
 Db 1031 TCTGATAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1090
 Qy 482 GCGCCAGTGAAGCTCAACGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
 Db 1091 CCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1150
 Qy 542 TCTTGTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
 Db 1151 TCTTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1210
 Qy 602 GCAGCAACGCGAGAGTCCAGGGCCAA 629
 Db 1211 GCCGCTTAAGGAGCGAGCCAGGGCCAA 1238

RESULT 5

US-08-194-338-1
 ; Sequence 1, Application US/08194338
 ; Patent No. 5474898
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, John C.
 ; APPLICANT: Frazer, Claire M.
 ; APPLICANT: McCombie, William R.
 ; TITLE OF INVENTION: OCTOPAMINE RECEPTOR
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear
 ; STREET: 620 Newport Center Drive, Sixteenth Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/194,338
 ; FILING DATE: 08-FEB-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/676,174
 ; FILING DATE: 28-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israel, Ned A.
 ; REGISTRATION NUMBER: 29,655
 ; REFERENCE/DOCKET NUMBER: NIH01.001DV1
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 235-8550
 ; TELEFAX: (619) 235-0176
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3335 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 319..2124
 ; US-08-194-338-1

Query Match 12.1%; Score 163.4; DB 1; Length 3335;
 Best Local Similarity 55.8%; Pred. No. 3.3e-23;
 Matches 351; Conservative 0; Mismatches 276; Indels 2; Gaps 2;

Qy 2 TGGACCAAGAGACCCCTACTCCGTGACAGCCAGCGGCCCATAGGGGGCCATCACT 61
 Db 611 TGGGCTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 670
 Qy 62 TCTCATCTCTTACCATCTTCTGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
 Db 671 TCATTATCTGCTGACATCATCTGGAACATCTGATGTTCTGATGTTTCACTTACA 730
 Qy 122 GCTGCTGCGCGCCCTCAGAACCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
 Db 731 AGCCGCTGGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 790
 Qy 182 TGGCCACGCTCATCTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
 Db 791 TGGCCCTTGGGCTGCGCTTCAAGTGGCTTACTGATCTGCGGCGGCTGGAGTTGG 850
 Qy 242 GCGCAGCTGCTGCGGAGTGTACTGCTGCGCTGAGCTGCTGCTTCTGCACTCTGCTCATG 301
 Db 851 GCATCAGCTGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 910
 Qy 302 TSCA-CTGTGCGCATCAGCTGCTGAGCGCTACTGCGCGGTGAGCGCGCTGAGTAC 360
 Db 911 TGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
 Qy 361 AACTCAGAGCGACCCCGCGCGCATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 970 GCCAGAAAGAGACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1029
 Qy 421 GCGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 Db 1030 TCTGATAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1089
 Qy 481 CCGCCCAAGTGAAGCTCAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Db 1090 GCGAGCGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1149
 Qy 541 TTTCTTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 Db 1150 TTTCTTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1209
 Qy 601 CGCAGCAACGCGAGAGTCCAGGGCCAA 629
 Db 1210 CGCGCTTAAGGAGCGAGCCAGGGCCAA 1238

RESULT 6

US-08-722-001-17
 ; Sequence 17, Application US/08722001
 ; Patent No. 576054
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Wayne J.
 ; APPLICANT: Huff, Joel R.
 ; APPLICANT: Nerenberg, Jennie B.

APPLICANT: Lee, Hee-Yoon
APPLICANT: Bell, Ian M.
TITLE OF INVENTION: ALPHALIC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-17
Query Match 11.7%; Score 158.6; DB 1; Length 921;
Best Local Similarity 57.0%; Pred. No. 2.4e-22;
Matches 312; Conservative 0; Mismatches 229; Indels 6; Gaps 1;
Db 63 CTTGATCTCTTTTACCATCTTTCGGCAACGCTTGTGATCTCTGCTGTGTGACCAACCG 122
170 CTTGATCTCTTTTGGCATCTGCGGCAACATCTAGTATCTTGTCTGTGGCTGGCAACCG 229
Qy 123 CTCGCTGGCGCCCTCAGAACCTGTCCTGTGCTGCGCGCGCGGCACATCTGT 182
Db 230 GCACCTGGAGAGCCCAACACTTATGTCAACTGGCCACATGCGGACCTGCTGT 289
Qy 183 GGCCACGCTCATCATCTCTTCTGCTGCGCAACGAGCTGTGGGCTAATGTAATTCCG 242
Db 290 GAGCTTACCGCTCTGCGCTTCTGAGCGCCCTAGAGGTGCTCGGCTAATGTAATTCCG 349
Qy 243 GCGCAGCTGTGCGAGGTGTACTGCGCTGAGCTGTCTTTCGACCTGTGCTCATCT 302
Db 350 GCGGATCTTCTGTGATCTGTGGGCAACGCTGTGCTGTGCAAGGCTCATCTCT 409
Qy 303 GCACCTGTGGCGCATCTGAGCGCTGAGCGCTGAGCGCGCGCTGAGTAACA 362
Db 410 GAGCTGTGGCGCATCTGATCTGATCTGATCTGAGGCTGTGCTGAGTAACA 469
Qy 363 CTCGACGCGCACCCCGCGCGCGCATCAAGTCAATCTCTGCTGTGCTGATGCGCGC 422
Db 470 CACGCTGTGATCCCGAGAGAGAGGCGCATCTTGGCCCTGCTGATGCTGTGCTGCTAC 529
Qy 423 CCGTATCTGTGCGCGCCCTTATCTACAAGGCGCAACAGCGCGCGCGCGCGCGCG 482
Db 530 CCGTATCTGTGCGCGCCCTTCTGCTGTGCTGAGAGAGCGCGCGCAACCGA-----CGATGA 583

483 CCCCAGTGAAGTCAACAGAGGCTGTGATCATCTGCGCTTCAGCATGCGATCTTT 542
584 CAGAGATGGCGGGTCTACCGAAGACCTCTTATGCGCTCTCTCTCTGCGCTCTT 643
Qy 543 CTTGCTCTTGGCTCTCATGATCTTGTCTACCTGCGCATCTACTGATTCGCAACG 602
Db 644 CTACATCCCTCTGCGGCTCATCTGATGATCTGCGCGCTGATATGATGCGCAAG 703
Qy 603 CAGCAAC 609
Db 704 AACCAAC 710
RESULT 7
US-08-722-001-24
Sequence 24, Application US/08722001
Patent No. 5760054
GENERAL INFORMATION:
APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel R.
APPLICANT: Nerenberg, Jennie B.
APPLICANT: Lee, Hee-Yoon
TITLE OF INVENTION: ALPHALIC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-24
Query Match 11.7%; Score 158.6; DB 1; Length 1567;
Best Local Similarity 57.0%; Pred. No. 2.5e-22;
Matches 312; Conservative 0; Mismatches 229; Indels 6; Gaps 1;
Db 63 CTTGATCTCTTTTACCATCTTTCGGCAACGCTTGTGATCTCTGCTGTGTGACCAACCG 122
170 CTTGATCTCTTTTGGCATCTGCGGCAACATCTAGTATCTTGTCTGTGGCTGGCAACCG 229
Qy 123 CTCGCTGGCGCCCTCAGAACCTGTCCTGTGCTGCGCGCGCGGCACATCTGT 182

Db	220	GCACCTGGCGGAGGCCCAACCACTACTTCAATGTGCAACCTGGCCATGCGCACTGCTGTT	288
Oy	183	GGCCACGCTCATCATCCCTTTCTCGCTGGCAACGAGCTGCTGGCTACTGTATCTTCCG	242
Db	290	GAGCTTACCCGCTCTGCGCCTTCTCAGCGGCGCTGAGAGTGTCTGGCTACTGGGTGTGGG	349
Oy	243	GGGCAAGGTGTGGAGGTGTACTCTGGCGCTCCAGCGTCTTTGTGACCTGTCCATCGT	302
Db	350	GGGAGCTTCTGTGACATCTGGGCAACCGGTGAGTGTCTGTGTGCAACAGCTTCATCTT	409
Oy	303	GCACTGTGTGGCCATCAGCCTGGACCGCTTACTGGGCGGTGAGCGCGCGCTGAGATCAA	352
Db	410	GAGCCTGTGGCGCATCTCATGATGGTGCATCATCGGGGTGGCTACTCTTGTCAAGTATCC	465
Oy	353	CTCCAAGCGCACCCCGCGCGCGCATCAAGTGATCATCTTCACTGTGTGCTCATTCGCCGC	422
Db	470	CACGCTGGTCAACCCGAGGAAAGGCATCTTGGCGCTGCTAGTGTGTGGGTCTTGTAC	529
Oy	423	CGTATCTTCGCTGCCGCCCTCATCTCAAGAGGCGACAGAGGCGCCCAAGCGCGCGGCG	482
Db	530	CGTCACTTCCATCTGGGCGCTCTCTTGGGTGGAAGAGCGCGCACCCAA-----CGATGA	583
Oy	483	CCCCAGTGCAGCTCAACAGAGAGGCGTGTATCATCTGTGGCTCTCCAGCATCGGATCTTT	542
Db	584	CAGAGAGTGGCGGGGTCAACCGAAGAACCTTCTATGCGCTTCTTCTCTTGGGGCTCTT	643
Oy	543	CTTTGCTCTTGGCTTCATCATGATCCCTGTCTACCTGCGCATCTACCTGATGCGCAACG	602
Db	644	CTACATCTCTCTGGCGGTATCTTACTCATGTACTCGCGGTCTTATATAGTGCCAAAG	703
Oy	603	CAGCAAC 609	
Db	704	AACCAAC 710	

RESULT 8
 US-08-334-698-3
 Sequence 3, Application US/08334698
 Patent No. 5556753
 GENERAL INFORMATION:
 APPLICANT: Jonathan A. Bard et al.
 TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
 TITLE OF INVENTION: Receptors and Uses Thereof
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: COOPER & DUNHAM
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/334,698
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/952,798
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 376901
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: (212) 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 3:

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? SEQUENCE CHARACTERISTICS:
? LENGTH: 1738 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: unknown
? MOLECULE TYPE: DNA (genomic)
? HYPOTHEICAL: N
? ANTI-SENSE: N
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 124..1683
? OTHER INFORMATION:
US-08-334-698-3
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RESULT 9
US-08-228-932-3
Sequence 3" Application US/08228932
Patent No. 5578611
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
TITLE OF INVENTION: PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,932
FILING DATE: 13-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-B/JPM/TEP
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-228-932-3

Query Match 11.6%; Score 157; DB 1; Length 1738;
Best Local Similarity 56.9%; Pred. No. 5.2e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

63 CCTCATCTCTTTACCATCTTTCGCAACGCTGCTGATCTCTGCTGTGTACACAGCCG 122
285 CTTTATCTCTTTGCGCATCTGCGCAACATCTATCTTGTGTGCGCTGCAACCG 344
123 CTGCGTGGCGCCGCTGAGAACCTGTTCTGTGTGCTGCGCGCGCGCAATCTGTGT 182
345 GCACCTGCGGACGCGCCACCACTTACTTGTGCACTGCTGCGCATGCGCACTGCTGT 404
183 GCGCAGCTCATATCTCTTTCTGCTGCGCAACGAGCTGCTGCGCTACTGTACTTCCG 242
405 GAGCTTACCGTCTGCTCTTCTGACGCGCGCTGAGAGTCTGCGCTACTGCGGTGGG 464
243 GCGCAGCTGCTGCGAGTGTACTGCGGCTGCGAGTCTCTTGTGCACTGCTGCTCATCT 302
465 GCGGATCTCTGTGACATCTGCGGACGCGTGTGATGTCTGTGTGCAACGCTTCATTTCT 524
303 GCACTGTGCGCATGACGCTGAGCGCTACTGCGCGCTGAGCGCGCGCTGAGTACAA 362
525 GAGCTGTGCGCATCTTCATCTGATGCTATGCGGAGTGGCTACTCTTGTGAGTATCC 584
363 CTCGACGCGACCGCGCGCGCATGAGTGCATCTGATCTGATGTGTGCTCATTCGCGC 422
585 CAGGCTGTGACCGCGGAGAAAGGCTCTTGGGCTGTCTGAGTGTCTGAGTCTTGTCTCAC 644
423 GGTATCTGCTGCGCGCGCTCTCATCTAAGGCGGACCAAGGCGCGCGCGCGCGGCG 482
645 GGTATCTGCTGCGCGCGCTCTCTTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 698
483 CCGCGAGTGAAGTGAAGCAAGAGGAGGCTGTGATCTGAGCTCTGAGCATTCGAGTCTTT 542
699 CAGAGAGTGTGGGAGTACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 758
543 CTTTGTCTTGTGCTCATGATCTTGTGTACTGCGCATCTGATCTGATCTGATCTGATCT 602

Db 759 CTACATCCCTCTGGCGGCTCATTTAGTCATGACTGCGGTGTCTATATATAGGCCAAGAG 818
QY 603 CAGCAAC 609
Db 819 AACCAAC 825

RESULT 10

US-08-468-939-3
Sequence 3, Application US/08468939
Patent No. 5714381
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-468-939-3

Query Match 11.6%; Score 157; DB 1; Length 1738;
Best Local Similarity 56.9%; Pred. No. 5.2e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

63 CCTCATCTCTTTACCATCTTTCGCAACGCTGCTGATCTCTGCTGTGTACACAGCCG 122
285 CTTTATCTCTTTGCGCATCTGCGCAACATCTATCTTGTGTGCGCTGCAACCG 344
123 CTGCGTGGCGCCGCTGAGAACCTGTTCTGTGTGCTGCGCGCGCGCAATCTGTGT 182
345 GCACCTGCGGACGCGCCACCACTTACTTGTGCACTGCTGCGCATGCGCACTGCTGT 404
183 GCGCAGCTCATATCTCTTTCTGCTGCGCAACGAGCTGCTGCGCTACTGTACTTCCG 242
405 GAGCTTACCGTCTGCTCTTCTGACGCGCGCTGAGAGTCTGCGCTACTGCGGTGGG 464
243 GCGCAGCTGCTGCGAGTGTACTGCGGCTGCGAGTCTCTTGTGCACTGCTGCTCATCT 302
465 GCGGATCTCTGTGACATCTGCGGACGCGTGTGATGTCTGTGTGCAACGCTTCATTTCT 524

Qy 303 GCACCTGTGCGGCATCAGCTGGACCGGCTCATGTGGCCGTGAGCGCGCTGGAGTACAA 3522

Db 555 GAGCCTGTGCGGCATCTTCATGCATGCTACATCGGAGGTGCGGTACTCTCTGAGATATCC 5844

Qy 363 CTCCAGGCGCACCCCGCGCCGCATCAAGTGCATCATCTCTCATGTGTGCTCATTCGCGC 4222

Db 585 CACGCTGGTGCATCCCGAGGAGAGGCCATCTTTGGCGCTGCTCAGTGTCTGGGCTTTGTTCAC 6444

Qy 423 CGTCATCTTGCCTGCGCGCCCTCATTTCAAGAGGCGACAGAGGCCGCCAGCGCGCGCGC 4822

Db 645 CGTCATCTTCATCGGCGCCTCTCTTGGGTGGAAGAGCGCGGACCCAA-----CGATGA 6988

Qy 483 CCCCCAGTGCAGAGTCTCAACAGAGAGCGCTGTGTATCATCTGTGGCCTTCCAGATCGGATCTTT 5422

Db 699 CAAGGAGTGCAGGCGGTACCGAAGAACCTTTTATAGCCCTTCTCTCTCTGTGGGCTCTTT 7588

Qy 543 CTTTGCTCTTGCCCTCATCATGATCTTGTGTATCTTGGCGCATTTACTGATTCGCCAAAGC 6022

Db 759 CTACATCTCCTCTGGCGCGTATTCTTAGTCAATGATCTGCCGTGTCTATATAGTGGCCAAAG 8188

Qy 603 CAGCAAC 609

Db 819 AACCAAC 825

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11 RESULT 11
12 US-08-406-855A-3
13 Sequence 3, Application US/08406855A
14 Patent No. 5861309
15 GENERAL INFORMATION:
16 APPLICANT: Jonathan A. Bard et al.
17 TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrennergic
18 TITLE OF INVENTION: Receptors and Uses Thereof
19 NUMBER OF SEQUENCES: 23
20 CORRESPONDENCE ADDRESS:
21 ADDRESSEE: Cooper & Dunham LLP
22 STREET: 1185 Avenue of the Americas
23 CITY: New York
24 STATE: New York
25 COUNTRY: U.S.A.
26 ZIP: 10036
27 COMPUTER READABLE FORM:
28 MEDIUM TYPE: Floppy disk
29 COMPUTER: IBM PC compatible
30 OPERATING SYSTEM: PC-DOS/MS-DOS
31 SOFTWARE: PatentIn Release #1.30
32 CURRENT APPLICATION DATA:
33 APPLICATION NUMBER: US/08/406,855A
34 FILING DATE: 21-AUG-1995
35 CLASSIFICATION: 435
36 ATTORNEY/AGENT INFORMATION:
37 NAME: White, John P.
38 REGISTRATION NUMBER: 28,678
39 REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE: (212) 278-0400
42 TELEFAX: (212) 391-0526
43 INFORMATION FOR SEQ ID NO: 3:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 1738 base pairs
46 TYPE: nucleic acid
47 STRANDEDNESS: single
48 TOPOLOGY: unknown
49 MOLECULE TYPE: DNA (genomic)
50 HYPOTHETICAL: N
51 ANTI-SENSE: N
52 FEATURE:
53 NAME/KEY: CDS
54 LOCATION: 124..1683
55 OTHER INFORMATION:
56 US-08-406-855A-3

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Query Match	Similarity	Score	DB 2:	Length
Match 311; Conservative	56.9%	Pred. No. 5.2e-22;	Indels 6;	Gaps 1
0;	Mismatches 230;			
11.6%;				
DB 2:				
Length 1738;				
Query	63	CCTCATCTCTTTTACCATCTTCGGCAACGGCTGTGTCATCTCGCTGTGTGTCACGACCG	1222	
Db	285	CTTATCTCTCTTTGGCCATCGTGGGCAACATCTTAGTCATCTTGTCTGTGGCTGCACCG	344	
Qy	123	CTCGTGTGGGCGCCCTCAGAACTCTTCTGTGTGTGCTGTGGCGCGCCGCAATCTGTGT	182	
Db	345	GCACCTGTGGAGCGCCACCAACTATTATGTCAACCTGGCCATAGCCGACCTGTGTGT	404	
Qy	183	GGCCACGCTCATCATCTCCCTTTCGCTGGGCCAAGAGCTGTGGGCTACTGTGATCTTCCG	242	
Db	405	GAGCTTACACGCTCTGCGCTTCTCTCAGCGGCCCTTAGAGTGCTCTGGCTACTGGGTGTGG	464	
Qy	243	GCGCAGGTGTGCGAGGTGTACTGTGGCGCTGCAGCTGCTCTTCTGTGACCTGTCCATCGT	302	
Db	465	GCGGATCTTCTGTGTGACATCTGTGGGACCGGTGTGATCTCTGTCTGCACAGCGCTCCATCT	524	
Qy	303	GCACCTGTGGCGCATCATCAGCTGTGACCGGCTACTGTGGGCCGTGAGCCGCGCTGAGATCAA	362	
Db	525	GAGCTGTGGCGCATCTCATCTGATGTGCTACATCGGGGCGCTACTCTCTGAGATGCC	584	
Qy	363	CTCCAAAGCGCACCCCGCGCGCATCAAGTGCATCATCTCACTGTGTGCTCATCGCCG	422	
Db	585	CACGCTGTGTACCCGGAGGAAGGCGCATCTTGGCGGTGTCAATGTCTGTGTGTCTGTCTCAG	644	
Qy	423	CGTCATCTGTGCTGCCGCCCTTCATTTACAAGGCGCAACAAGGCGCCCGCAGCGCGGGCG	482	
Db	645	CGTCATCTTCCATCGGGCCCTCTCTCTTGGGTGGAAGAGCGCGGACCCCA-----CGATGA	698	
Qy	483	CCCCAAGTGCAGCTCAACAGGAGGCGCTGTATCATCTGCGCTCCAGCATCGGATCTTT	542	
Db	659	CAGGAGTGTGGGGGTACCGAAGAACCTTTCTATGCGCTCTTCTCTCTGTGGGCTCTTT	758	
Qy	543	CTTGTGCTCTTGCCCTCATGATCTTGTCTTACTGCTGGGCATCTACCTGATGCCAAGCG	602	
Db	759	CTACATCTCTCTGCGGCTCATCTTGTATGTATGTATGTATGTATGTATGTATGTATGTATGT	818	
Qy	603	CAGCAGAC 609		
Db	819	AACGACC 825		

RESULT 12
US-08-722-190-3
Sequence 3, Application US/08722190
Patent No. 5990128
GENERAL INFORMATION:
APPLICANT: Charles Giuchowski, Carlos C. Forray, George
Applicant: Chiu, Theresa A. Branche, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,190
FILING DATE: 4-APR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.

REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1738 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: N
 ANTI-SENSE: N
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 124..1683
 OTHER INFORMATION:
 US-08-722-190-3

Query Match 11.6%; Score 157; DB 2; Length 1738;
 Best Local Similarity 56.9%; Pred. No. 5.2e-22;
 Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

QY 63 CCTATTCTTTTACCATCTTGGCAAGCTGTGATCCTGGCTGTGTAACAGCCG 122
 DB 285 CTTATCTCTTTGGCATGTGGCAACATCTAGTATCTGTCTGTGGCCGCAACCG 344
 QY 123 CTCGCTGGGCGCCCTGAGAACCTGTCCTGCTGCTGCGCCCGCGCAATCTGGT 182
 DB 345 GCACCTGGGAGCGCCCAACCACTTATGTCAACCTGCGCAATGCGCCGCTGCTT 404
 QY 183 GAGCAAGCTCATCTCTTCTGCTGGCAAGAGCTGCTGGCTACTGTAATCTTCCG 242
 DB 405 GAGCTTACCGCTCTGCGCTTCTCAGGCGCCCTAGAGTCTCTGCTAGTGGTCTGG 464
 QY 243 GCGGACGTGTGAGAGGTGTAAGTGGCTGAGCTGCTCTTGTGCACTGTCATCTGT 302
 DB 465 GCGGATCTTGTGATCATCTGGGAGCGCTGATGTCCTGTGCAAGCGTCCATCTCT 524
 QY 303 GCACCTGTGGCCATCAGCTGAGCGCTACTGCGGCGGTGAGCGGCGCTGAGTACAA 362
 DB 525 GAGCTGTGGGCAATCTCCATCATCTGCTGAGGAGGCTGCTCTGTGAGTATCC 584
 QY 363 CTCGAAGCGACCCCGCGCGCATCAAGTGCATCTTCACTGTGTGCTGATGCGCGC 422
 DB 585 CAGCTGTGACCCCGAGAGGAGGCACTTGGCGCTGCAAGTGTGCTGTGTCCAC 644
 QY 423 CGTCACTGTGCGCGCCCTCATCTAACAAGGCGCAAGGCGCCCGCGCGGCGG 482
 DB 645 CGTCACTGTGCGCGCTCTCTTGGGTGGAAGGAGCGGCAACCA-----CGATGA 698
 QY 483 CCCCCAGTGAAGCTCAACGAGAGGCTGTGATCATCTGAGCTCGAGCATCGATCTTT 542
 DB 699 CAAAGAGTGGGGGTCAAGAGAACCTTCTATGCGCTCTCTCTCTGAGGCTCTTT 758
 QY 543 CTTTGCTCTGCTGCTCATATGATCTTGTCTTACTGCGCATCTAAGTATGCCAAG 602
 DB 759 CTACATCTCTGTGGCGGTATCTAGTCACTGCGGTGTATATAGTGGCAAGAG 818
 QY 603 CAGCAAC 609
 DB 819 AACCAAC 825

RESULT 13
 US-08-244-354-3
 ; Sequence 3, Application US/08244354
 ; Patent No. 6015819
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Gluchowski, et al.
 ; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO

TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: COOPER & DUNHAM LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/244,354
 FILING DATE: April 1, 1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1738 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: N
 ANTI-SENSE: N
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 124..1683
 OTHER INFORMATION:
 US-08-244-354-3

Query Match 11.6%; Score 157; DB 3; Length 1738;
 Best Local Similarity 56.9%; Pred. No. 5.2e-22;
 Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

QY 63 CCTATTCTTTTACCATCTTGGCAAGCTGTGATCCTGGCTGTGTAACAGCCG 122
 DB 285 CTTATCTCTTTGGCATGTGGCAACATCTAGTATCTGTCTGTGGCCGCAACCG 344
 QY 123 CTCGCTGGGCGCCCTGAGAACCTGTCCTGCTGCTGCGCCCGCGCAATCTGGT 182
 DB 345 GCACCTGGGAGCGCCCAACCACTTATGTCAACCTGCGCAATGCGCCGCTGCTT 404
 QY 183 GAGCAAGCTCATCTCTTCTGCTGGCAAGAGCTGCTGGCTACTGTAATCTTCCG 242
 DB 405 GAGCTTACCGCTCTGCGCTTCTCAGGCGCCCTAGAGTCTCTGCTAGTGGTCTGG 464
 QY 243 GCGGACGTGTGAGAGGTGTAAGTGGCTGAGCTGCTCTTGTGCACTGTCATCTGT 302
 DB 465 GCGGATCTTGTGATCATCTGGGAGCGCTGATGTCCTGTGCAAGCGTCCATCTCT 524
 QY 303 GCACCTGTGGCCATCAGCTGAGCGCTACTGCGGCGGTGAGCGGCGCTGAGTACAA 362
 DB 525 GAGCTGTGGGCAATCTCCATCATCTGCTGAGGAGGCTGCTCTGTGAGTATCC 584
 QY 363 CTCGAAGCGACCCCGCGCGCATCAAGTGCATCTTCACTGTGTGCTGATGCGCGC 422
 DB 585 CAGCTGTGACCCCGAGAGGAGGCACTTGGCGCTGCAAGTGTGCTGTGTCCAC 644
 QY 423 CGTCACTGTGCGCGCCCTCATCTAACAAGGCGCAAGGCGCCCGCGCGGCGG 482
 DB 645 CGTCACTGTGCGCGCTCTCTTGGGTGGAAGGAGCGGCAACCA-----CGATGA 698

QY 483 CCCCCAGTCAAGCTCAACGAGGCGCTGTACATCTGGCCCTCCAGATCGGATCTTT 542
| | | | |
DB 699 CAAAGAGTCGGGGTCAACGAGAACCTTCTATGCTCTCTCTCTGGGCTCTT 758
| | | | |
QY 543 CTTTGCTCTTGCTCATCATGATCTTGTCTTACCTGGCATCTACTATCGCCAAAG 602
| | | | |
DB 759 CTACATCCCTCTGGCGGCTATCTAGTCACTGCTCGGTCTATATAGTGGCAAG 818
| | | | |
QY 603 CAGCAAC 609
| | | | |
DB 819 AACCAAC 825
| | | | |
RESULT 14
US-09-206-899-3
; Sequence 3, Application US/09206899
; Patent No. 6083705
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,899
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,855
; FILING DATE: 21-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1683
; OTHER INFORMATION:
; US-09-206-899-3
Query Match 11.6%; Score 157; DB 3; Length 1738;
Best Local Similarity 56.9%; Pred. No. 5.2e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;
QY 63 CCGCATCTCTTACCATCTCTGGCAACGCTCTGCTGATCTCTGGCTGTACCGCG 122
| | | | |
DB 285 CTTGATCCCTCTTGGCCATCTGGGCAACATCTTATGTCATCTGTCTGTGCGCTGCAACG 344
| | | | |
QY 123 CTCGCTGCGCGCCCTCAGAACCTGTCTCTGTGTGCTGTGCGCGCGCGCAACATCTGGT 182
| | | | |

DB 345 GCACCTGCGAGACCCCAACCACTACTTCACTGTCAACCTGGCCAGCGGACCTGCTTT 404
| | | | |
QY 183 GGCACAGCTCATCATCCCTTTCTGCTGACCAAGAGCTGTGGCTACTGTGATCTTCCG 242
| | | | |
DB 405 GAGCTTCAACCTCTGCTCTTCTTCAAGGCGCCCTTAAGAGTGTCTGCTACTTGGGTGTGG 464
| | | | |
QY 243 GCGCAGTGTGTGAGGTGATCTGAGCTGTGAGCTGTCTTCTGACCTGTGATCGT 302
| | | | |
DB 465 GCGGATCTTCTGTGACATCTGGGCAAGCGGTGATGTCTGTCTGACAGCGCTTCATCTT 524
| | | | |
QY 303 GCACCTGTGCGGCTCATAGCTGTGACCGCTACTGTGGCCCGGACCGCGCTGTGATCA 362
| | | | |
DB 525 GAGCTGTGCGGCTCATCTGATCATGATCGATCAATCGGAGCGCTTACTCTGTCAATATCC 584
| | | | |
QY 363 CTCGAAGCAGCCCGCGCGCATCAAGTCAATCTCACTGTGTGCTATCGCGCG 422
| | | | |
DB 585 CAGCTGTGATCCCGGAGGAGGAGCCATCTTGGCGCTGTCAAGTGTGTGGGTCTTGTCCAG 644
| | | | |
QY 423 CGTCAATCTGCTGCGCGCCCTTCATCTACAGGAGCGACCAAGGCGCCCGCGCGCG 482
| | | | |
DB 645 CGTCAATCTCATCTGCGGCTCTCTTGGGTGGAAGAGCGCGCACCCAA-----CGATGA 698
| | | | |
QY 483 CCCCCAGTCAAGCTCAACGAGGCGCTGTACATCTTGGCTCTCAGCATGTGATCTTT 542
| | | | |
DB 699 CAAAGAGTCGGGGTCAACGAGAACCTTCTATGCTCTCTCTCTCTGCGGCTCTT 758
| | | | |
QY 543 CTTTGCTCTTGCTCATCATGATCTTGTCTTACCTGCGGATCTACCTGATGCGCAAG 602
| | | | |
DB 759 CTACATCCCTCTGGCGGCTATCTAGTCACTGCTGCGGTCTATATAGTGGCAAG 818
| | | | |
QY 603 CAGCAAC 609
| | | | |
DB 819 AACCAAC 825
| | | | |

RESULT 15
US-09-444-783-3
; Sequence 3, Application US/09444783
; Patent No. 6420389
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, et al.
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,783
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-09-444-783-3

Query Match 11.6%; Score 157; DB 4; Length 1738;
Best Local Similarity 56.9%; Pred. No. 5.2e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

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Search completed: February 8, 2004, 01:28:47
Job time : 96.7987 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 20:38:27 ; Search time 516.217 Seconds
(without alignments)
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Title: US-09-692-077D-1

Perfect score: 1353

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Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1351.4	99.9	1353	9	US-09-825-923-3
3	1351.4	99.9	1353	15	US-10-077-870-3
4	1349.8	99.8	2072	12	US-10-305-720-1181
5	1349.8	99.8	3274	15	US-10-225-567A-41
6	1325	97.9	1344	15	US-10-001-073-2
7	1323.4	97.8	1344	9	US-09-825-923-1
8	1323.4	97.8	1344	15	US-10-077-870-1
9	600.2	44.4	6904	13	US-10-311-455-48
10	512.6	37.9	6904	13	US-10-311-455-47
11	458.4	33.9	1386	15	US-10-001-073-40
12	448.8	33.2	1374	15	US-10-001-073-42
13	447.2	33.1	2826	15	US-10-225-567A-43
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16	443	32.7	1350	15	US-10-001-073-25	Sequence 25, Appl
17	442.4	32.7	3653	15	US-10-225-567A-39	Sequence 39, Appl
18	441.4	32.6	1350	15	US-10-001-073-24	Sequence 24, Appl
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23	157	11.6	1738	12	US-10-305-720-1402	Sequence 3, Appl
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25	157	11.6	1738	15	US-10-238-129-3	Sequence 3, Appl
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27	157	11.6	1786	15	US-10-225-567A-35	Sequence 35, Appl
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36	142.6	10.5	2048	14	US-10-052-589-1	Sequence 1, Appl
37	141	10.4	1548	15	US-10-054-616A-8	Sequence 8, Appl
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40	138.4	10.2	1098	13	US-09-826-509-430	Sequence 430, Ap
41	138.4	10.2	1930	12	US-10-305-720-1171	Sequence 1171, Ap
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44	138.2	10.2	1639	15	US-10-238-129-5	Sequence 5, Appl
45	138.2	10.2	1639	15	US-10-238-667-5	Sequence 5, Appl

ALIGNMENTS

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Sequence 1, Application US/10001073					
GENERAL INFORMATION:					
APPLICANT: Liggett, Stephen					
APPLICANT: Small, Kirsten					
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms					
FILE REFERENCE: 13073-PCT					
CURRENT APPLICATION NUMBER: US/10/001, 073					
CURRENT FILING DATE: 2001-11-01					
NUMBER OF SEQ ID NOS: 53					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 1					
LENGTH: 1353					
TYPE: DNA					
ORGANISM: Homo sapiens					
US-10-001-073-1					
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Best Local Similarity 100.0%; Pred. No. 0;					
Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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 RESULT 2
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 ; Sequence 3, Application US/09825923
 ; Patent No. US2001001638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Snapir, Amir
 ; APPLICANT: Heinonen, Paula
 ; APPLICANT: Alhopuro, Pia
 ; APPLICANT: Karvonen, Matti
 ; APPLICANT: Koulu, Markku
 ; APPLICANT: Pesonen, Ulla-Mari
 ; APPLICANT: Scheinin, Mika
 ; APPLICANT: Salonen, Jukka T
 ; APPLICANT: Tuominen, Tomi-Pekka
 ; APPLICANT: Lakka, Timo A
 ; APPLICANT: Nyyssönen, Kristina
 ; APPLICANT: Salonen, Riitta
 ; APPLICANT: Kauppinen, Jussi
 ; APPLICANT: Valkonen, Veli-Pekka
 ; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
 ; FILE REFERENCE: protein, and uses thereof
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: US/09/825,923
 ; PRIOR FILING DATE: 2000-05-25
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1353
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1350)
 ; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
 ; OTHER INFORMATION: protein
 ; US-09-825-923-3
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; Publication No. US20030003470A1
; GENERAL INFORMATION:

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; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077, 870
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3
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Query Match 99.9%; Score 1351.4; DB 15; Length 1353;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||
Qy 721 GCTTCTGCAGAGAGGTCAAAGCACTGAGTCTCACTGGGAGAGAGAGGGAG 780
Db 721 GCTTCTGCAGAGAGGTCAAAGCACTGAGTCTCACTGGGAGAGAGAGGGAG 780
|||
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Query Match      99.8%; Score 1349.8; DB 12; Length 2072;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGCACACGAGACCCCTACTCCGTCGACAGGCTCCACAGGSCCATAGAGGCGGCATATACC 60
413 ATGAGCACACGAGACCCCTACTCCGTCGACAGGCTCCACAGGSCCATAGAGGCGGCATATACC 472

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QY	61	TTCTCATTTCTCTTTTACATCTTGGGCAACGCTGATCATCTGGCTGTGACAGC	120
Db	473	TTCTCATTTCTCTTTTACATCTTGGGCAACGCTGTGATCATCTGGCTGTGACAGC	5322
QY	121	CGCTGCTCGGCGCCCTCAGAACCTGTTCCGAGTCCGTGGCCCGCCGCAATCTCG	180
Db	533	CGCTGCTCGGCGCCCTCAGAACCTGTTCTGGAGTCCGTGGCCCGCCGCAATCTCG	592
QY	181	GTGGCAGGCTATATATCCCTTTCTCGTGGCCAAAGAGCTGTGGGCTACTGTACTTC	240
Db	593	GTGGCAGGCTATATATCCCTTTCTCGTGGCCAAAGAGCTGTGGGCTACTGTACTTC	652
QY	241	CGGCGCAGGTGGTGGAGGTGTACTGGCGTGGAGTGTCTTTCTTCTTCTGACCTTGTCAATC	300
Db	653	CGGCGCAGGTGGTGGAGGTGTACTGGCGTGGAGTGTCTTTCTTCTTCTGACCTTGTCAATC	712
QY	301	GTGCACTGTGGGCGCATCAAGCTGTGACCGCTTCTGGGCGGTGAGCCGCGCTGGAGTATC	360
Db	713	GTGCACTGTGGGCGCATCAAGCTGTGACCGCTTCTGGGCGGTGAGCCGCGCTGGAGTATC	772
QY	361	AACTCCAGCGCACCCCGCGCGCATCAAGTGCATATCTCACTGTGTGGCTCATCCGC	420
Db	773	AACTCCAGCGCACCCCGCGCGCATCAAGTGCATATCTCACTGTGTGGCTCATCCGC	480
QY	421	GCGCTCATCTCGGCGCGCGCCCTCATCTTCAAGGGCGACCAAGGCCCCCAGCGCGCGG	832
Db	833	GCGCTCATCTCGGCGCGCGCCCTCATCTTCAAGGGCGACCAAGGCCCCCAGCGCGCGG	892
QY	481	CGCCCCAGGTGCAGTCTCAACCAAGAGGCTGTGATCATCTGGCCCTCAGATGGATCT	540
Db	893	CGCCCCAGGTGCAGTCTCAACCAAGAGGCTGTGATCATCTGGCCCTCAGATGGATCT	952
QY	541	TTCTTTGCTCTTGTGCTCATCATGATCCCTTGTCTTACTCTGGCATCTACTGATGCCAA	600
Db	953	TTCTTTGCTCTTGTGCTCATCATGATCCCTTGTCTTACTCTGGCATCTACTGATGCCAA	1012
QY	601	CGAGAGAACCGCAAGTCCAGAGGCCCAAGAGGGGGGCTGGGACAGGTGAGTCCAGACAG	660
Db	1013	CGAGAGAACCGCAAGTCCAGAGGCCCAAGAGGGGGGCTGGGACAGGTGAGTCCAGACAG	1072
QY	661	CCCCGACCCGACATGTGTGGGCTTTTGGCCCTCAAGCCAAATCTGCCAGCTGTGCTGTGT	720
Db	1073	CCCCGACCCGACATGTGTGGGCTTTTGGCCCTCAAGCCAAATCTGCCAGCTGTGCTGTGT	1132
QY	721	GCTTCTGCGCAGAGGTCAATCGACACTCGAAGTCCACTGGGAGAGAGAGAGGGAGAG	780
Db	1133	GCTTCTGCGCAGAGGTCAATCGACACTCGAAGTCCACTGGGAGAGAGAGAGGGAGAG	1192
QY	781	ACCCCTGAAGATCTGAGGACCCGGGCTTTGCGACCCAGTTTGGCTGGCCCTTTCCCAACTCA	840
Db	1193	ACCCCTGAAGATCTGAGGACCCGGGCTTTGCGACCCAGTTTGGCTGGCCCTTTCCCAACTCA	1252
QY	841	GGCCAGGGCCAGAGAGGGTGTGTTTGTGGGCAATCTTCAAGAGATGAAGCTGAAGAGAG	900
Db	1253	GGCCAGGGCCAGAGAGGGTGTGTTTGTGGGCAATCTTCAAGAGATGAAGCTGAAGAGAG	1312
QY	901	GAAAGAGAGAGAGAGAGAGAGATGTGAACCCAGGCGAGTCCAGTGTCTTCCGGCC	960
Db	1313	GAAAGAGAGAGAGAGAGAGAGATGTGAACCCAGGCGAGTCCAGTGTCTTCCGGCC	1372
QY	961	TCAAGCTTGAGCCCGCCGCTGCAAGACGCAAGGGCTTCCGGGTGCTGGCCACCTTACGT	1020
Db	1373	TCAAGCTTGAGCCCGCCGCTGCAAGACGCAAGGGCTTCCGGGTGCTGGCCACCTTACGT	1432
QY	1021	GGCAGAGTCTCTTGGGACAGGGGCTGTGGTGTATATGATGGGACAGTGTGGCTTCAAGG	1080
Db	1433	GGCAGAGTCTCTTGGGACAGGGGCTGTGGTGTATATGATGGGACAGTGTGGCTTCAAGG	1492
QY	1081	GGCAGACTAACCCGGAGAGAGGCTTCAACTTGTGCTGTGCTGTGTGATCTTGGCGTTTTT	1140
Db	1493	GGCAGACTAACCCGGAGAGAGGCTTCAACTTGTGCTGTGCTGTGTGATCTTGGCGTTTTT	1552

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QY 1141 GTGCTCTGCTGGTTCCTCCCTTCTCTTCTTCTGAGCTCAAGACCCGCGGCGCATCTGGCCGAAGAC 1200
Db 1553 GTGCTCTGCTGGTTCCTCCCTTCTCTTCTTCTGAGCTCAAGACCCGCGGCGCATCTGGCCGAAGAC 1612
QY 1201 TGCAGAGTGCCCAATGAGCTCTTCCAGTTCCTTCTTGATCGGCTACATGCAAGACTCA 1260
Db 1613 TGCAGAGTGCCCAATGAGCTCTTCCAGTTCCTTCTTGATCGGCTACATGCAAGACTCA 1672
QY 1261 CTGAACCTGTATTATCTACACCATCTTCAACGAGACTTCGCGCTGCTTCCGAGAGATC 1320
Db 1673 CTGAACCTGTATTATCTACACCATCTTCAACGAGACTTCGCGCTGCTTCCGAGAGATC 1732
QY 1321 CTGTGCGCGCCGTGGACCCAGACGCGCTGTGA 1353
Db 1733 CTGTGCGCGCCGTGGACCCAGACGCGCTGTGA 1765

RESULT 5
US-10-225-567A-41
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41

Query Match 99.8%; Score 1349.8; DB 15; Length 3274;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGCAACACGAGACCCCTTACTCTCGGTGCAAGCGGCGCCATAGCGGCGCATCAAC 60
Db 1 ATGAGCAACACGAGACCCCTTACTCTCGGTGCAAGCGGCGCCATAGCGGCGCATCAAC 60
QY 61 TTCTCATATTTCTTTAACCATCTTGGGCAACGCTCTGTGATCTCTGTGTGAACAGC 120
Db 61 TTCTCATATTTCTTTAACCATCTTGGGCAACGCTCTGTGATCTCTGTGTGAACAGC 120
QY 121 CGCTGCTGCGCGGCCCTCAGAACCTGTTCCGTGAGTGTGCTGAGCGCGCGCGACATCTGT 180
Db 121 CGCTGCTGCGCGGCCCTCAGAACCTGTTCCGTGAGTGTGCTGAGCGCGCGCGACATCTGT 180
QY 181 GTGGCAGCGCTCATCATCCCTTTCGTGCTGGCCAAAGAGCTGTGGGCTACTGGTATCTC 240
Db 181 GTGGCAGCGCTCATCATCCCTTTCGTGCTGGCCAAAGAGCTGTGGGCTACTGGTATCTC 240
QY 241 CGGCGCAAGTGTGTGAGAGTGTACTGTGCGCTCGACGTGTCTTTTGTGACCTCTGTCAATC 300
Db 241 CGGCGCAAGTGTGTGAGAGTGTACTGTGCGCTCGACGTGTCTTTTGTGACCTCTGTCAATC 300
QY 301 GTGCACTGTGTGGCCATCAGCTTGAGACGCTTACTGTGGCCGTGAGCGCGCTGAGATAC 360
Db 301 GTGCACTGTGTGGCCATCAGCTTGAGACGCTTACTGTGGCCGTGAGCGCGCTGAGATAC 360
QY 361 AACTTCAGACGCAACCCCGCGCGCATCAAGTGCATCATCTTCACTGTGTGTGCTCATTCGC 420
Db 361 AACTTCAGACGCAACCCCGCGCGCATCAAGTGCATCATCTTCACTGTGTGTGCTCATTCGC 420
QY 421 GCGGTGATCTGCTGTGCGCGCCCTTACTTAAAGAGGCGACAGAGGCCCAAGCGCGCGG 480

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Db      421  GCGGTGATCTGGCTGCGCGCCCTTATCTAACAAAGGGGAGCAAGAGGCCCCAGCGCGCGG 480
Oy      481  CGCCCCCAGTGGAAAGCTCAACCAAGAGGCGCTGGTACATCTGGCTCCAGCATCGGATCT 540
Db      481  CGCCCCCAGTCAAGCTCAACCAAGAGGCGCTGGTACATCTGGCTCCAGCATCGGATCT 540
Oy      541  TTCTTTGGCTCCTGGCTCATCATCATGATCCCTGGCTCACTCGGGGATCTACCTGGCCAA 600
Db      541  TTCTTTGGCTCCTGGCTCATCATCATGATCCCTGGCTCACTCGGGGATCTACCTGGCCAA 600
Oy      601  CGCAGCAACCCGACAGAGTCCCAAGGCGCAAGAGGGGGGCGCTGGCAGGGTGAAGTCCAA 660
Db      601  CGCAGCAACCCGACAGAGTCCCAAGGCGCAAGAGGGGGGCGCTGGCAGGGTGAAGTCCAA 660
Oy      661  CCCCCGACCCGACCATGTGGTGGGGCTTTGGCTCAGCCCAACTGCGCAGCCCTTGCTGTG 720
Db      661  CCCCCGACCCGACCATGTGGTGGGGCTTTGGCTCAGCCCAACTGCGCAGCCCTTGCTGTG 720
Oy      721  GCTTCTGCGACAGAGAGTCAACGGAACCTCGAAGTCACTGGGGGAGAGAGAGAGGGGGAG 780
Db      721  GCTTCTGCGACAGAGAGTCAACGGAACCTCGAAGTCACTGGGGGAGAGAGAGAGGGGGAG 780
Oy      781  ACCCTTGAAAGATCTGGGACCCGGGCGCTTGCCAGCCAGTTGGGGCTGCGCTCCCACTCA 840
Db      781  ACCCTTGAAAGATCTGGGACCCGGGCGCTTGCCAGCCAGTTGGGGCTGCGCTCCCACTCA 840
Oy      841  GGCCGAGGCGCCAGAAAGAGGGGTGTTTGTGGGGGACATCTCCAGAGATGAAGCTGAAGAG 900
Db      841  GGCCGAGGCGCCAGAAAGAGGGGTGTTTGTGGGGGACATCTCCAGAGATGAAGCTGAAGAG 900
Oy      901  GAAAGAGAGAGAGAGAGAGAGAGAAAGTGAACCCCAAGGCAAGTGCAGTGTCTCCGGCC 960
Db      901  GAAAGAGAGAGAGAGAGAGAGAGAAAGTGAACCCCAAGGCAAGTGCAGTGTCTCCGGCC 960
Oy      961  TCAGCTTGCAGGCCCCCGCGCTGACAGAGCCAGAGGCTCCGGGGTGTGTGACCACTTACGT 1020
Db      961  TCAGCTTGCAGGCCCCCGCGCTGACAGAGCCAGAGGCTCCGGGGTGTGTGACCACTTACGT 1020
Oy      1021  GGCCGAGTGTCTCTTGGGGCAAGGGGCGTGGGTCTATAGTGGGCAAGTGTGGCTCGAAGG 1080
Db      1021  GGCCGAGTGTCTCTTGGGGCAAGGGGCGTGGGTCTATAGTGGGCAAGTGTGGCTCGAAGG 1080
Oy      1081  GCGCAGCTGACCCCGGAGAAAGGGCTTACCTTCGTCGTGGCTGTGTGCAATGGGCGTTTTT 1140
Db      1081  GCGCAGCTGACCCCGGAGAAAGGGCTTACCTTCGTCGTGGCTGTGTGCAATGGGCGTTTTT 1140
Oy      1141  GNGCTGTGTGGTGGTCCCTCTTCTTTCAGCTACAGGCTGGGCGGCATCTGCGCGGAAGCAC 1200
Db      1141  GNGCTGTGTGGTGGTCCCTCTTCTTTCAGCTACAGGCTGGGCGGCATCTGCGCGGAAGCAC 1200
Oy      1201  TGCAGAGTGGCCCATGAGGCTCTTTCAGATCTTCTTCGATCGGCTAAGTCAAGACTCA 1260
Db      1201  TGCAGAGTGGCCCATGAGGCTCTTTCAGATCTTCTTCGATCGGCTAAGTCAAGACTCA 1260
Oy      1261  CTGAACCTCTGTTATCTACACCATCTTCAACCAAGAGATTCCGCGGTGCTTCCGGAAGATC 1320
Db      1261  CTGAACCTCTGTTATCTACACCATCTTCAACCAAGAGATTCCGCGGTGCTTCCGGAAGATC 1320
Oy      1321  CTGTGCGCGCGCTGGAACCCAGACGGGCTGTGTGA 1353
Db      1321  CTGTGCGCGCGCTGGAACCCAGACGGGCTGTGTGA 1353

RESULT 6
US-10-001-073-2
; Sequence 2, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT

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/ CURRENT APPLICATION NUMBER: US/10/001.073
/ CURRENT FILING DATE: 2001-11-01
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 1344
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-001-073-2

Query Match      97.9%; Score 1325; DB 15; Length 1344;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 1 ATGACACACGAGAGCCCTACTCCGTCAGAGCCACAGCCGCGCATAGCGGCGCATACC 60
DB 1 ATGACACACGAGAGCCCTACTCCGTCAGAGCCACAGCCGCGCATAGCGGCGCATACC 60
QY 61 TTCCTCATTTCTTTACCATCTTCGCGACGCTCTGGTCACTCTGGCTGTGTGACACAG 120
DB 61 TTCCTCATTTCTTTACCATCTTCGCGACGCTCTGGTCACTCTGGCTGTGTGACACAG 120
QY 121 CGCTCGCTGCGCCCTCTCAAACTGTTCTGTGTGCTGCGCCGCGCGCATCTG 180
DB 121 CGCTCGCTGCGCCCTCTCAAACTGTTCTGTGTGCTGCGCCGCGCGCATCTG 180
QY 181 GTGACACGCTCATCATCTCTTCTGCTGCGCCACAGAGCTGTGGGCTACTGTACTTC 240
DB 181 GTGACACGCTCATCATCTCTTCTGCTGCGCCACAGAGCTGTGGGCTACTGTACTTC 240
QY 241 CGGCGACGTCGTGCGAGGTGTACTGCGCGCTGACGCTGCTTCTTTCACCTGTCATC 300
DB 241 CGGCGACGTCGTGCGAGGTGTACTGCGCGCTGACGCTGCTTCTTTCACCTGTCATC 300
QY 301 GTGACACTGTGCGCCATCAGCTTCGACCGCTACTGCGCGCTGAGCCGCGCTGAGTAC 360
DB 301 GTGACACTGTGCGCCATCAGCTTCGACCGCTACTGCGCGCTGAGCCGCGCTGAGTAC 360
QY 361 AACTCCAAAGGCGACCCCGCGCGCATCAAGTGCATCATCTCTGCTGTGAGCTCATCGCC 420
DB 361 AACTCCAAAGGCGACCCCGCGCGCATCAAGTGCATCATCTCTGCTGTGAGCTCATCGCC 420
QY 421 GCGGTATCTGCTGCGCCCTCATCTACAGGCGACCAAGGCGCCCGACCGCGCGG 480
DB 421 GCGGTATCTGCTGCGCCCTCATCTACAGGCGACCAAGGCGCCCGACCGCGCGG 480
QY 481 CGGCCCCAGTGCAGAGCTCAACAGAGGCGCTGTGTACTCTGCTTCAGCATCGATCT 540
DB 481 CGGCCCCAGTGCAGAGCTCAACAGAGGCGCTGTGTACTCTGCTTCAGCATCGATCT 540
QY 541 TTCTTTGCTCTGCTCATCATGATCTGTGTACTGCTGCGCATCTACCTGATCGCCAA 600
DB 541 TTCTTTGCTCTGCTCATCATGATCTGTGTACTGCTGCGCATCTACCTGATCGCCAA 600
QY 601 CGGAGCAACCGAGAGGTCCAGAGGCGCAAGGCGGCGCTGCGAGGAGTGTCAAGCAG 660
DB 601 CGGAGCAACCGAGAGGTCCAGAGGCGCAAGGCGGCGCTGCGAGGAGTGTCAAGCAG 660
QY 661 CCCCCAGCCGACATGTGTGGGCTTTGGCTTCAGCCAAATGCAACCTTGCGCTCTGTG 720
DB 661 CCCCCAGCCGACATGTGTGGGCTTTGGCTTCAGCCAAATGCAACCTTGCGCTCTGTG 720
QY 721 GCTTTCGAGAGAGGTCAACGAGCACTGGAATCTCACTGGGAGAGAGGAGGAGGAG 780
DB 721 GCTTTCGAGAGAGGTCAACGAGCACTGGAATCTCACTGGGAGAGAGGAGGAGGAG 780
QY 781 ACCCTTGAAGATATCTGAGACCCGCGCTTGCACCCAGTGTGGCTGCTTCCCACTCA 840
DB 781 ACCCTTGAAGATATCTGAGACCCGCGCTTGCACCCAGTGTGGCTGCTTCCCACTCA 840
QY 841 GCGCAGGCGCAGAGAGGAGGAGTGTGTGTGGGCTATCTTCAGAGATGAAGAGAG 900
DB 841 GCGCAGGCGCAGAGAGGAGGAGTGTGTGTGGGCTATCTTCAGAGATGAAGAGT----- 891
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QY 901 GAAGAGAGAGAGAGAGAGAGAGTGAACCCAGGCGAGTGCAGTGTCTCCGCC 960
DB 892 GAAGAGAGAGAGAGAGAGAGAGTGAACCCAGGCGAGTGTCTCCGCC 951
QY 961 TCAGCTTGAGGCCCCCGCTGAGAGACCAAGGCTCCCGGAGTGTGAGCCACTTACGT 1020
DB 952 TCAGCTTGAGGCCCCCGCTGAGAGACCAAGGCTCCCGGAGTGTGAGCCACTTACGT 1011
QY 1021 GCGCAGTGTCTCTGAGGAGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
DB 1012 GCGCAGTGTCTCTGAGGAGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1071
QY 1081 GCGCAGTGTCTCTGAGGAGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
DB 1072 GCGCAGTGTCTCTGAGGAGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1131
QY 1141 GTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
DB 1132 GTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1191
QY 1201 TGCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
DB 1192 TGCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1251
QY 1261 CTGAACCTGTATCTACACCATCTTCAACAGAGCTTCGCGCGCTTCCGAGAGATC 1320
DB 1252 CTGAACCTGTATCTACACCATCTTCAACAGAGCTTCGCGCGCTTCCGAGAGATC 1311
QY 1321 CTGTGCGCGCGCTGAGACCGAGCGGCTGTGTGA 1353
DB 1312 CTGTGCGCGCGCTGAGACCGAGCGGCTGTGTGA 1344
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RESULT 7
US-09-825-923-1
/ Sequence 1, Application US/09825923
/ Patent No. US20010016338A1
/ GENERAL INFORMATION:
/ APPLICANT: Snapir, Amir
/ APPLICANT: Heinonen, Paula
/ APPLICANT: Alhopuro, Pia
/ APPLICANT: Karvonen, Matti
/ APPLICANT: Koulou, Markku
/ APPLICANT: Pesonen, Ullamari
/ APPLICANT: Scheinin, Mika
/ APPLICANT: Salonen, Jukka T
/ APPLICANT: Tuomala, Tomi-Pekka
/ APPLICANT: Lakka, Timo A
/ APPLICANT: Myllynen, Kristina
/ APPLICANT: Salonen, Riitta
/ APPLICANT: Kananen, Jussi
/ APPLICANT: Valonen, Veli-Pekka
/ TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
/ FILE REFERENCE: Alpha-2B-AR variant
/ CURRENT APPLICATION NUMBER: US/09/825,923
/ PRIOR APPLICATION NUMBER: 09/422,985
/ PRIORITY FILING DATE: 2000-05-25
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1344
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: CDS
/ LOCATION: (1) (1341)
/ OTHER INFORMATION: Coding sequence for variant human
/ OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1
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Query Match 97.8%; Score 1323.4; DB 9; Length 1344;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 ATGGACACCAAGAGACCCCTTACTCCGTGACAGGCCCAAGCGGCATAGCGGGGCATACACC 60
DB 1 ATGGACACCAAGAGACCCCTTACTCCGTGACAGGCCCAAGCGGCATAGCGGGGCATACACC 60
QY 61 TTCCTATTCTCTTTACATCTTCCGCAAGCTCTGAGTCACTCTGGCTGTGTGACACAG 120
DB 61 TTCCTATTCTCTTTACATCTTCCGCAAGCTCTGAGTCACTCTGGCTGTGTGACACAG 120
QY 121 CGCTGCTGCGCGCCCTTCAAGAACTGTTCTGAGTGTGCTGAGCGCGCCGCAATCTTG 180
DB 121 CGCTGCTGCGCGCCCTTCAAGAACTGTTCTGAGTGTGCTGAGCGCGCCGCAATCTTG 180
QY 181 GTGGCCAGCTCATATCCCTTTCTGCTGAGCCCAAGAGTGTGGGCTACTGTACTTC 240
DB 181 GTGGCCAGCTCATATCCCTTTCTGCTGAGCCCAAGAGTGTGGGCTACTGTACTTC 240
QY 241 CGGCGCAGCTGTGCGAGGCTGATCTGAGGCTGAGCTGCTTCTGCACTCTGCTCATC 300
DB 241 CGGCGCAGCTGTGCGAGGCTGATCTGAGGCTGAGCTGCTTCTGCACTCTGCTCATC 300
QY 301 GTGCACTGTGCGCATCAAGCTTGAACCGCTTACCTGAGCGCGCTGAGTAC 360
DB 301 GTGCACTGTGCGCATCAAGCTTGAACCGCTTACCTGAGCGCGCTGAGTAC 360
QY 361 AACTCCAGGCGCAACCCCGCGCGCATCAAGTGCATCATCTCTGCTGCTCATGCC 420
DB 361 AACTCCAGGCGCAACCCCGCGCGCATCAAGTGCATCATCTCTGCTGCTCATGCC 420
QY 421 GCGCTATCTGCTGCGCGCCCTTCAATCTCAAGGGGACAGGGCCCGCGCGCGG 480
DB 421 GCGCTATCTGCTGCGCGCCCTTCAATCTCAAGGGGACAGGGCCCGCGCGCGG 480
QY 481 CCGCCCGCAGTGCAGCTCAACAGAGGCTGTATCTCTGCTCTCCAGATCGATCT 540
DB 481 CCGCCCGCAGTGCAGCTCAACAGAGGCTGTATCTCTGCTCTCCAGATCGATCT 540
QY 541 TTCTTTGCTCTTGCCTCATCATGATCTTTGCTTACCTGCGCATCTGATCGCCAA 600
DB 541 TTCTTTGCTCTTGCCTCATCATGATCTTTGCTTACCTGCGCATCTGATCGCCAA 600
QY 601 CCGCAGAACCGCAGAGTCCCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 601 CCGCAGAACCGCAGAGTCCCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 661 CCGCAGAACCGCAGAGTCCCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
DB 661 CCGCAGAACCGCAGAGTCCCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 721 GCTTTGCGCAGAGGCTCAACCGCACTCGAAGTCCACTGCGGAGAAAGAGAGGAG 780
DB 721 GCTTTGCGCAGAGGCTCAACCGCACTCGAAGTCCACTGCGGAGAAAGAGAGGAG 780
QY 781 ACCCTGAAAGATCTGAGGACCCGCGGCTTGCACCAAGTTGGCTCCCTTCCCACTA 840
DB 781 ACCCTGAAAGATCTGAGGACCCGCGGCTTGCACCAAGTTGGCTCCCTTCCCACTA 840
QY 841 GGCAGAGGCGCAGAGAGGAGTGTGAGGAGGATCTCAAGAGATGAAGTGAAGAG 900
DB 841 GGCAGAGGCGCAGAGAGGAGTGTGAGGAGGATCTCAAGAGATGAAGTGAAGAG 900
QY 901 GAAAGAGAGAGAGAGAGAGAGTGTGAACCCCAAGCAAGTGCAGTGTCTCCGAGC 960
DB 901 GAAAGAGAGAGAGAGAGAGAGTGTGAACCCCAAGCAAGTGCAGTGTCTCCGAGC 960
QY 961 TCAAGCTTGAAGCCCCCGCTGACAGCCCAAGAGGCTCCCGGCTGTGACCACTTAC 1020
DB 961 TCAAGCTTGAAGCCCCCGCTGACAGCCCAAGAGGCTCCCGGCTGTGACCACTTAC 1020
QY 1021 GGCAGAGTCTCTGTGGCAGGGGCGTGGGCTGATAGTGGGAGTGTGGGTCAAG 1080
DB 1021 GGCAGAGTCTCTGTGGCAGGGGCGTGGGCTGATAGTGGGAGTGTGGGTCAAG 1080

DB 1012 GGCAGAGTCTCTGTGGCAGGGGCGTGGGCTGATAGTGGGAGTGTGGGTCAAG 1071
QY 1081 GGCAGAGTCTCTGTGGCAGGGGCGTGGGCTGATAGTGGGAGTGTGGGTCAAG 1140
DB 1072 GGCAGAGTCTCTGTGGCAGGGGCGTGGGCTGATAGTGGGAGTGTGGGTCAAG 1131
QY 1141 GTGCTGTGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
DB 1132 GTGCTGTGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1191
QY 1201 TGCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1260
DB 1192 TGCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1251
QY 1261 CTGAACCTCTTATCTTCAACCACTTCTTCAACCACTTCTTCAACCACTTCTTCAAC 1320
DB 1252 CTGAACCTCTTATCTTCAACCACTTCTTCAACCACTTCTTCAACCACTTCTTCAAC 1311
QY 1321 CTGTGCGCGCGCGTGAACCGCAGAGCGGCTGTGA 1353
DB 1312 CTGTGCGCGCGCGTGAACCGCAGAGCGGCTGTGA 1344

RESULT 8
US-10-077-870-1
; Sequence 1, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

Query Match 97.8%; Score 1323.4; DB 15; Length 1344;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 ATGGACACCAAGAGACCCCTTACTCCGTGACAGGCCCAAGCGGCATAGCGGGGCATACACC 60
DB 1 ATGGACACCAAGAGACCCCTTACTCCGTGACAGGCCCAAGCGGCATAGCGGGGCATACACC 60
QY 61 TTCCTATTCTCTTTACATCTTCCGCAAGCTCTGAGTCACTCTGGCTGTGTGACACAG 120
DB 61 TTCCTATTCTCTTTACATCTTCCGCAAGCTCTGAGTCACTCTGGCTGTGTGACACAG 120
QY 121 CGCTGCTGCGCGCCCTTCAAGAACTGTTCTGAGTGTGCTGAGCGCGCCGCAATCTTG 180
DB 121 CGCTGCTGCGCGCCCTTCAAGAACTGTTCTGAGTGTGCTGAGCGCGCCGCAATCTTG 180
QY 181 GTGGCCAGCTCATATCCCTTTCTGCTGAGCCCAAGAGTGTGGGCTACTGTACTTC 240
DB 181 GTGGCCAGCTCATATCCCTTTCTGCTGAGCCCAAGAGTGTGGGCTACTGTACTTC 240
QY 241 CGGCGCAGCTGTGCGAGGCTGATCTGAGGCTGAGCTGCTTCTGCACTCTGCTCATC 300
DB 241 CGGCGCAGCTGTGCGAGGCTGATCTGAGGCTGAGCTGCTTCTGCACTCTGCTCATC 300
QY 301 GTGCACTGTGCGCATCAAGCTTGAACCGCTTACCTGAGCGCGCTGAGTAC 360
DB 301 GTGCACTGTGCGCATCAAGCTTGAACCGCTTACCTGAGCGCGCTGAGTAC 360

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Db      | 301 GTGCACTTGGCCATCAGCTCGACCGCTGAGTCCGCGGCTGAGTAC 360
Qy      | 361 AACTCAAGGCGACCCCGCGCGCATCAGTCACTCTCTGTGTCTATCGCC 420
Db      | 361 AACTCAAGGCGACCCCGCGCGCATCAGTCACTCTCTGTGTCTATCGCC 420
Qy      | 421 GCGGTATCTGCTGCGCGCGCATCTCTCAAGGCGCGCGCGCGCGCGG 480
Db      | 421 GCGGTATCTGCTGCGCGCGCATCTCTCAAGGCGCGCGCGCGCGCGG 480
Qy      | 481 CGCGCCAGTGCAGAGCTCAACGAGAGCGCTGTGTATACCTCTCCAGATCGATCT 540
Db      | 481 CGCGCCAGTGCAGAGCTCAACGAGAGCGCTGTGTATACCTCTCCAGATCGATCT 540
Qy      | 541 TTCTTTGCTCTCTGCTCTCATCATGATCTCTGTCTACCTGCGCATCTACCTGATCGCAAA 600
Db      | 541 TTCTTTGCTCTCTGCTCTCATCATGATCTCTGTCTACCTGCGCATCTACCTGATCGCAAA 600
Qy      | 601 CGGAGAACCGGAGAGGTCCGAGGCGCAAGGCGGCGCTGTGTGTGATCGAAGCAG 660
Db      | 601 CGGAGAACCGGAGAGGTCCGAGGCGCAAGGCGGCGCTGTGTGTGATCGAAGCAG 660
Qy      | 661 CCCGACCCGACCATGCTGTGCGGCTTTGCTCTCAAGCAAGCTGCGAGCGCTGCTGTGT 720
Db      | 661 CCCGACCCGACCATGCTGTGCGGCTTTGCTCTCAAGCAAGCTGCGAGCGCTGCTGTGT 720
Qy      | 721 GCTTCTGCGAGAGAGTCAACGAGCACTCGAAGTCCACTGTGGGAGAGAGAGAGAGAG 780
Db      | 721 GCTTCTGCGAGAGAGTCAACGAGCACTCGAAGTCCACTGTGGGAGAGAGAGAGAGAG 780
Qy      | 781 ACCCTGAAAGATCTGAGGAGCCCGGCGCTTGCACCCGAGTGGGCTGCTTCCCACTCA 840
Db      | 781 ACCCTGAAAGATCTGAGGAGCCCGGCGCTTGCACCCGAGTGGGCTGCTTCCCACTCA 840
Qy      | 841 GGCAGAGGCGCAGAGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db      | 841 GGCAGAGGCGCAGAGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Qy      | 901 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db      | 901 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy      | 961 TCAAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db      | 961 TCAAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy      | 1021 GGCAGAGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db      | 1021 GGCAGAGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy      | 1081 GCGCAGCTGACCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db      | 1081 GCGCAGCTGACCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy      | 1141 GTGCTGTGAGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db      | 1141 GTGCTGTGAGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Qy      | 1192 TGCAAGGTGCGCCATGAGCTCTTTCAGTCTCTTGTGATCGGCTACTCAACAGCTCA 1251
Db      | 1192 TGCAAGGTGCGCCATGAGCTCTTTCAGTCTCTTGTGATCGGCTACTCAACAGCTCA 1251
Qy      | 1261 CTGAACCTCTGTATCTACAGCATCTTCAACAGAGACTTCCGCGTGTGCTTCCGAGAGATC 1320
Db      | 1261 CTGAACCTCTGTATCTACAGCATCTTCAACAGAGACTTCCGCGTGTGCTTCCGAGAGATC 1320
Qy      | 1321 CTGTGCGCGCGTGTGAGACCAAGAGCGCGCTGTGA 1353
Db      | 1321 CTGTGCGCGCGTGTGAGACCAAGAGCGCGCTGTGA 1353
Qy      | 1312 CTGTGCGCGCGTGTGAGACCAAGAGCGCGCTGTGA 1344
Db      | 1312 CTGTGCGCGCGTGTGAGACCAAGAGCGCGCTGTGA 1344
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US-10-311-455-48/c
; Sequence 48, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIERENBERG, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 48
; LENGTH: 6904
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: 821
; OTHER INFORMATION: n is a or g or c or t
US-10-311-455-48
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Query Match 44.4%; Score 600.2; DB 13; Length 6904;
Best Local Similarity 75.8%; Pred. No. 1.2e-137;
Matches 759; Conservative 0; Mismatches 233; Indels 9; Gaps 1;

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Qy      | 1 ATGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db      | 1904 ATGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1845
Qy      | 61 TTCTCTATCTCTTTTAAACATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db      | 1844 TTCTCTATCTCTTTTAAACATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1785
Qy      | 121 CGCTGCTGCGGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db      | 1784 CGCTGCTGCGGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1725
Qy      | 181 GTGAGCAGCTCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db      | 1724 ATGAGCAGCTCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1665
Qy      | 241 CGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db      | 1664 CGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1605
Qy      | 301 GTGCACTGTGCGCATCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db      | 1604 GTGCACTGTGCGCATCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1545
Qy      | 361 AACTCAAGGCGACCCCGCGCGCATCAAGTGTATATCTCTCACTGTGTGTGTGTGTGTGTGTGTGT 420
Db      | 1544 AACTCAAGGCGACCCCGCGCGCATCAAGTGTATATCTCTCACTGTGTGTGTGTGTGTGTGTGTGT 1485
Qy      | 421 GCGGTATCTGCTGCGCGCGCATCTCTCAAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db      | 1484 GCGGTATCTGCTGCGCGCGCATCTCTCAAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425
Qy      | 481 CGCGCCAGTGCAGAGCTCAACGAGAGCGCTGTGTATACCTCTGCGATCGATCTGATCT 540
Db      | 1424 CGCGCCAGTGCAGAGCTCAACGAGAGCGCTGTGTATACCTCTGCGATCGATCTGATCT 1365
Qy      | 541 TTCTTTGCTCTCTGCTCTCATCATGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db      | 541 TTCTTTGCTCTCTGCTCTCATCATGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
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/ CURRENT FILING DATE: 2001-11-01
 / NUMBER OF SEQ ID NOS: 53
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 40
 / LENGTH: 1386
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 US-10-001-073-40

Query Match	33.9%;	Score 458.4;	DB 15;	Length 1386;
Best Local Similarity	62.6%;	Pred. No. 6.7e-103;		
Matches 829; Conservative	0;	Mismatches 411;	Indels 84;	Gaps 4

[illegible]

OY	913	GAGAGAGAGAGAGATGTGTAAACCCAGAGGACATGCTCAGTGTCTCCGACCTCAGCTTCAGC	972
Db	967	GCGAGGCTCGGAGGCGGCTGAATGTGGGGGCGCTTACCGCTCCAGGTGCCCGGGCCCGGT	1026
OY	973	CCCCCGCTGACAGACCCACAGGGCTCCCGGCTGTGACCACCTTACGTGCCAGGTGTCT	1032
Db	1027	GGCCGCTCTCGGCGCCAGACTGCGCTCCGTGAGATCTTCTTCGTGCGCCCGGCGCGG	1086
OY	1033	CTGGGACAGGGGCGTGGGTGCTATATAGGTGGGCAATGGTGGCGTCTGAAAGGGGCGACGTACC	1092
Db	1087	GCGGCGACAGCGT-----GTGCGCCGCGCAAGTGTGGCCAGGGC	1125
OY	1093	CGGAGAAAGCGCTTCACTTTCGTGCTGGCTGTGGTCAATTGGCGTTTGTGTCTGTCTGG	1152
Db	1126	CGCAGAAAGGCTTCACTTTGTGTCTGGCTGTGGTCAATGGGCGGTTCGTGTCTGTCTGG	1185
OY	1153	TTCCCTTCTTCTTCACTACGTACAGCTTGGGGCCATCTGGCCCGAAGCACTGCAAGGTGCC	1212
Db	1186	TTCCCTTCTTCTTCACTTACAGCTTGTACGGCATCTTGGCCGCGAGGCTTCCAGGTGCC	1245
OY	1213	CATGGCGCTTCCAGTTCCTTCTTGATGGGCTACTGCAACAGCTCACTGAACCTGT	1272
Db	1246	GGCCGCTTTCAAAGTTCTTCTTGATGGGCTACTGCAACAGCTCGCTCAACCCGAGTC	1305
OY	1273	ATCTACACCATCTTCAACACAGACTTCCGCGCTGCCCTTCGAGAGATCTGTGCGGCGG	1332
Db	1306	ATCTACACGGTCTTCAACACAGATTTCCGCGCATCTTCAAGACACATCTCTTCCGACGG	1365
OY	1333	TGGA	1336
Db	1366	AGGA	1369

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RESULT 12
US-10-001-073-42
; Sequence 42, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic re
; FILE REFERENCE: 13073-Pct
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 1374
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-42

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Query Match	33.2%	Score 448.8	DB 15	Length 1374
Best Local Similarity	62.4%	Pred. No. 1.5e-105		
Matches 826	Conservative 0	Mismatches 402	Indels 96	Gaps 4
Qy	13	GACCCCTACTCCGTGACGAGCCACAGGCGCCATAGCGGCGCCATACCTTCTCCTAATTC	72	
Db	130	GGCCTAGTACTCGGCGCGCGCGCGGTGGGACAGGCGTGGCTGCGCGGTGGCGCTTCTCCTACATGTC	189	
Qy	73	TTTACCATCTTGGGCAACGCTCTGGGTATCTGATCTGATTTGATACGACCGCTGCTGGC	132	
Db	190	TTTACCGTGTGGGCAACGCTGCTGGTGTGATGCGCGTCTGTACGACGCGGCGCTGGCTGC	249	
Qy	133	GCCCTCAAGAACTGTTCTCTGGTGTGCTGGCGCCGCGGACATCCTGGTGGCAACGCTC	192	
Db	250	GCGCCACAGAACTCTTCCGTGGTGTGCTGGCGCTCGGCGGACATCTGGTGGCAACGCTG	309	
Qy	193	ATGATCCCTTCTCGCTGGGCAACGAGCTGTGGGCTACTGTATCTTCGGGCGCACTGG	252	
Db	310	GTCATGCGCTTCTCGTGTGGCAACGAGCTCATGAGCTACTGTGATCTTCGGGCGAGGTGG	369	
Qy	253	TGGAGGTGTACTGGCGGCTCGACAGCTGCTTTGTGACCTCGGCATCGGCACTGTGC	312	

DB 370 TGGGGGCTGACCTGGCGCTGATGCTGTTTGGACCTCGGATCGGATCTGTGT 429
QY 313 GCCATAGCGCTGAGCGGCTACTGGGCGGAGCGCGGCTGGAGTCAACCTCAAGCGC 372
DB 430 GCCATAGCGCTGAGCGGCTACTGGGCGGAGCGCGGCTGGAGTCAACCTCAAGCGC 489
QY 373 ACCCGCGCGGCTGATCAAGTGCATCTCTCATGTGTGCTCATCGCGCGCTCATCTCG 432
DB 490 AACACACGCGCGCTCAAGGCGACCATCTGTGCGGTGTGCTCATCTCGCGCTCATCTCG 549
QY 433 CTGCGCGCGCTCATCTCAAGGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 492
DB 550 TTCCCGCGCGCTGTCT---CGCTCAAGCGGACCGGCGCGCGCGCGCGCGCGCGCGCG 606
QY 493 AAGCTCAACGAGAGCGGCTGATCATCTGCGCTTCCAGATCGGATCTTTCTTGTCTCT 552
DB 607 GGCCTCAAGAGACGAGACCTGTGATCTGTCTCTCTGATCGGCTCTTCTTCTGCGCGC 666
QY 553 TGCCTCATGATGATCTTGTCTCTCTGCGCTCATCTGATCTGCGCAACGCGCAACCGC 612
DB 667 TGCCTCATGATGAGCTTGTGTCTACGCGCGCTCATCTGATGATGCGCAAGCGTGCAGCGC 726
QY 613 AAGAGTCCAGGCGCAAGGCGGCGCTGCGCAGGCTGAGTCCAGAGCGCGCGCGCGCGAG 672
DB 727 A-----CGCTCAGCGAGAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 759
QY 673 CATGTGGGGCTTTGGCGCTCAGCCAACTGCGAGCGCGCTGCGCTCTGTGCTTGTGCAAG 732
DB 760 GACGGGTGCTCCCGGCTACCGAAACGCGGCTGCGCGCGCGCGCGCGCGCGCGCGAGAC 819
QY 733 GAGGTCAAGGAGACCTCGAAGTCCACTGCGGAGAGAGAGAGGAGGAGAGAGAGAGAG 792
DB 820 GGGCACTGGCGAG 879
QY 793 ACTGGAGCCCGGCGCTTGGCAACCAAGTTGGGCTGCCCTTCCAACTCAGGCGCGCGAG 852
DB 880 AAGCGGCGCGC-----GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 853 AAGGAGGTGTTTGTGGGCTCTCCAGAGATGAAAGTGAAGAGAGAGAGAGAGAGAGAG 912
DB 901 TTGGCGCGGCG 960
QY 913 GAGGAGAGAGAGAGTGTGAACCCAGGAGAGTGCAGTGTCTCGCGCTCAGCTTTCAGC 972
DB 961 CAGGCGCGGCTGAGTGGGCGCGCTGACCGCTCCAGGTCCTCGGCGCGCGCGCGCGCG 1020
QY 973 CCGCGCGCTCAGGAGCGCACAGGCGCTCCGCGGTGCTGCGCAACCTCAGTGCAGTGTCTC 1032
DB 1021 CTCTGCG 1080
QY 1033 CTGGGCGAGGCGCTGGGTGCTATAGTGGGCAAGTGTGGCGTGAAGGCGCGAGCTGACC 1092
DB 1081 ACGAGC-----GTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1113
QY 1093 CGGAGAGAGCGCTTCACTTGTGCTGCGGTGATGAGTGTGCTTGTGCTGCTGCTGCTG 1152
DB 1114 CGCGAGAGAGCGCTTCACTTGTGCTGCGGTGATGAGTGTGCTTGTGCTGCTGCTGCTG 1173
QY 1153 TTCCCGCTTCTTCACTCAAGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1212
DB 1174 TTCCCGCTTCTTCACTCAAGCGCTGAGCGATGCGCGAGGCGCTGCGAGGTGCGC 1233
QY 1213 CATGCGCTTCTTCAAGTGTCTTCTGAGTGGCTACTGCAACGCTCACTGAACTGCTT 1272
DB 1234 GCGCGCGCTTCAAGTGTCTTCTGAGTGGCTACTGCAACGCTCACTGAACTGCTT 1293
QY 1273 ATCTACAGCTTCAACGAGAGCTTCCGCGCTGCTGCGAGAGTCTCTGCGCGCGCG 1332
DB 1294 ATCTACAGGCTTCAACGAGAGTTCGCGCGCATCTTCAAGAGCATCTCTTCTGCGAG 1353
QY 1333 TGGAG 1336
|||

DB 1354 AGGA 1357
RESULT 13
US-10-225-567A-43
; Sequence 43, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-43
Query Match 33.1%; Score 447.2; DB 15; Length 2826;
Best Local Similarity 62.6%; Pred. No. 4,2e-100;
Matches 829; Conservative 0; Mismatches 408; Indels 87; Gaps 5;
QY 13 GACCCCTACTCCGTGAGGCGCACAGCGGCGCATAGCGGCGCGCATCTTCTCTATCTTC 72
DB 1021 GGCAGTACTCG 1080
QY 73 TTACCATCTTGGCGAACGCTGTGTGATCTGTGCTGTGTGAACAGCGCGCTGCTGCGC 132
DB 1081 TTACCGGTGTGGCGAACGCTGTGTGATCTGTGATCGCGTGTGACAGCGCGCGCGCGCG 1140
QY 133 GCCCTCAGAACCTGTCTGT 192
DB 1141 GCGCACAGAACCTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
QY 193 ATCATCCCTTCTCTGCTGCGCAACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 252
DB 1201 GTCTAGCGCTTCTCTGT 1260
QY 253 TCGAGGTGTACTGTGCGCTGTGACGTCTTCTGTGACCTGTGTGTGTGTGTGTGTGTGT 312
DB 1261 TCGGGGTGTACTGTGCGCTGTGACGTCTTCTGTGACCTGTGTGTGTGTGTGTGTGTGT 1320
QY 313 GCCATGAGCTGTGACCGCTACTGTGGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCG 372
DB 1321 GCCATGAGCTGTGACCGCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
QY 373 ACCCGCGCGCGCATCAAGTGCATCTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 432
DB 1381 AACACAGCGCGCTCAAGGCGCACATCTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 433 CTGCGCGCGCTCATCTCAAGGCGGAGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 492
DB 1441 TTCCCGCGCGTGTCT---CGCTCAAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1497
QY 493 AAGCTCAACGAGAGCGCTGTGATCTGTGCGCTTCCAGATGAGTCTTCTTGTGTCTCT 552
DB 1498 GGCCTCAAGAGAGCGCTGTGATCTGTGCGCTTCCAGATGAGTCTTCTTGTGTCTCT 1557
QY 553 TGCCTCATGATGATCTTGT 612
DB 1558 TGCCTCATGATGAGCTTGT 1617
QY 613 AAGAGTCCAGGCGCAAGGCGGCGCGCTGCGGCAAGGTGTGTGTGTGTGTGTGTGTGTGT 672
DB 1618 A-----CGCTCAGCGAGAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1667

Db 1083 AGCAGC-----GTGTGCGCGCGCAAGGCGCCAGGCG 1115
Qy 1093 CGGGAAGAGCGCTTCACTTGTGCTGCGTGTGATGATGAGCGCTTTTGTGCTGTGCG 1152
Db 1116 CGGGAAGAGCGCTTCACTTGTGCTGCGTGTGATGATGAGCGCTTTTGTGCTGTGCG 1175
Qy 1153 TTCCCTCTTCTTCACTTCAAGCGCTGCGCGCATCTGCGCGAAGCACTGCAAGTGGCC 1212
Db 1176 TTCCCTCTTCTTCACTTCAAGCGCTGCGCGCATCTGCGCGAAGCACTGCAAGTGGCC 1235
Qy 1213 CATGCGCTTCTTCAAGTCTTCTTGTGATGCGCTACTGCAAGCTCACTGAACCTGT 1272
Db 1236 GCGCGCGCTCTTCAAGTCTTCTTGTGATGCGCTACTGCAAGCTCACTGAACCTGT 1295
Qy 1273 ATCTACACATCTTCAACCAAGACTTCCGCGCGCTCTCCGAGATCTCTGCGCGCG 1332
Db 1296 ATCTACACAGTCTTCAACCAAGACTTCCGCGCGCTCTTCAAGCAATCTCTTCCGAG 1355
Qy 1333 TCGA 1336
Db 1356 AGGA 1359

RESULT 15
US-10-101-510-754
; Sequence 754, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: MAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 754
; LENGTH: 1382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-754

Query Match 32.8%; Score 444; DB 13; Length 1382;
Best Local Similarity 62.2%; Pred. No. 2.3e-99;
Matches 823; Conservative 0; Mismatches 405; Indels 96; Gaps 4;

Qy 13 GACCCCTACTCGGTGAGCGCAAGCGCGCATAGCGCGCCATCACTTCTCATTTCT 72
Db 132 GGCAGACTCTCGCGCGCGCGGTGCGAGGCGTGGCTGCGGTGGCTTCTCATCTGTC 191
Qy 73 TTACCATCTTGGCAAGCGCTGTGATCTGCTGCTGTGTGACAGCGCGCTGTGCGC 132
Db 192 TTACCATCTTGGCAAGCGCTGTGATCTGCTGCTGTGTGACAGCGCGCGCTGTGCGC 251
Qy 133 GCGCCCTCAAGACTGTTCTGTGTGCTGCGCGCGCGCGCAATCTGTGTGCGCAAGCT 192
Db 252 GCGCCCTCAAGACTGTTCTGTGTGCTGCGCGCGCGCGCAATCTGTGTGCGCAAGCT 311
Qy 193 ATCATCTCTTCTGCTGCGCGCAAGCGCTGTGCGCTACTGTGATCTTCTGCGCGAGTGG 252
Db 312 GTCATCTCTTCTGCTGCGCGCAAGCGCTGTGCGCTACTGTGATCTTCTGCGCGAGTGG 371
Qy 253 TCGAGAGTGTACTGTGCGCGCTGAGTGTCTTCTGCAAGCTGTGCACTGTGCGCTGTGCG 312
Db 372 TCGAGAGTGTACTGTGCGCGCTGAGTGTCTTCTGCAAGCTGTGCACTGTGCGCTGTGCG 431
Qy 313 GCCATGAGCTGTGAGCGCTACTGTGAGCGCGCGCGCTGTGAGTCAACTTCAAGCGC 372
Db 432 GCCATGAGCTGTGAGCGCTACTGTGAGCGCGCGCGCTGTGAGTCAACTTCAAGCGC 491

Qy 373 ACCCGCGCGCATCAAGTGCATCATCTCACTGTGTGCTCATCGCCCGCTCATCTCG 432
Db 492 ACACACAGCGCGCTTCAAGGCGCACATCTGTGCGGTGTGCTCATCTCGCGCTCATCTCG 551
Qy 433 CTGCGCGCGCTCATCTCAAGGCGCACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 492
Db 552 TTCCCGCGCGCTGTCT---CGCTTACCGCGCACGCGCGCGCGCGCGCGCGCGCGCGCG 608
Qy 493 AAGCTCAACAGAGGCGCTGTATCATCTGTGCGCTTCCAGATCGGATCTTCTTGTGCTCT 552
Db 609 GCGCTCAACAGAGCGCTGTATCATCTGTGCGCTTCTTCAAGGCGCGCGCGCGCGCGCGCG 668
Qy 553 TGCCTCATGATGATCTTGTCTTCACTGTGCGCATCTTCACTGCAAGCGCAAGCGCAAGCG 612
Db 669 TGCCTCATGATGATGATCTTGTCTTCACTGTGCGCATCTTCACTGCAAGCGCAAGCGCG 728
Qy 613 AGAGTCCCAAGGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 672
Db 729 A-----CGCTTCAAGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 761
Qy 673 CATGTGCGCGCTTGTGCGCTCAAGCAAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 732
Db 762 GACGTGCGCTTGTGCGCTTGTGCGCTTGTGCGCTTGTGCGCTTGTGCGCTTGTGCGCG 821
Qy 733 GAGTCAACGAGCACTCAAGTGTCACTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
Db 822 GCGCATGTGCG 881
Qy 793 ACTGAGACCGCGCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 852
Db 882 AGCGCGCGCG-----GCGCGCGCGCG 902
Qy 853 AAGGAGAGGCTTGTGCGCGCATCTCAAGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAG 912
Db 903 TTGCG 962
Qy 913 GAGGAGAGAGAGAGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 972
Db 963 GAGGAGAGAGAGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1022
Qy 973 CCG 1032
Db 1023 CTGTGCG 1082
Qy 1033 CTGCGGAGAGGCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1092
Db 1083 AGCAGC-----GTGTGCGCGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCG 1115
Qy 1093 CGGGAAGAGCGCTTCACTTGTGCTGCGTGTGATGATGAGCGCTTTTGTGCTGTGCG 1152
Db 1116 CGGGAAGAGCGCTTCACTTGTGCTGCGTGTGATGATGAGCGCTTTTGTGCTGTGCG 1175
Qy 1153 TTCCCTCTTCTTCACTTCAAGCGCTGCGCGCATCTGCGCGAAGCACTGCAAGTGGCC 1212
Db 1176 TTCCCTCTTCTTCACTTCAAGCGCTGCGCGCATCTGCGCGAAGCACTGCAAGTGGCC 1235
Qy 1213 CATGCGCTTCTTCAAGTCTTCTTGTGATGCGCTACTGCAAGCTCACTGAACCTGT 1272
Db 1236 GCGCGCGCTCTTCAAGTCTTCTTGTGATGCGCTACTGCAAGCTCACTGAACCTGT 1295
Qy 1273 ATCTACACATCTTCAACCAAGACTTCCGCGCGCTCTCCGAGATCTCTGCGCGCG 1332
Db 1296 ATCTACACAGTCTTCAACCAAGACTTCCGCGCGCTCTTCAAGCAATCTCTTCCGAG 1355
Qy 1333 TCGA 1336
Db 1356 AGGA 1359

Search completed: February 8, 2004, 01:46:18
Job time : 529.717 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 7, 2004, 20:15:32 / Search time 3132.92 Seconds
(Without alignments)
10496.265 Million cell updates/sec

Title: US-09-692-077d-1

Perfect score: 1353

Sequence: 1 atgaccaccagagaccctca.....ggaccaccagagcctgtga 1353

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST:
1: em_ests:
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3: em_ests:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	654.4	48.4	872	29	AL606560 Horse alp
2	513.2	37.9	1044	13	BO880026 AGENCOURT
3	442.4	32.7	2410	11	BC035047 Homo sapi
4	390.6	28.9	3594	11	AK046802 Mus muscu

Result No.	Score	Query Match	Length	ID	Description
5	324	23.9	1201	9	AL544609
6	322.4	23.8	1201	9	AL530418
7	295.4	21.8	988	13	BO887729 AGENCOURT
8	278.4	20.6	691	10	BB643669
9	278.4	20.6	2736	11	AK046211
10	267.2	19.7	909	14	CA477609
11	262.6	19.4	677	28	B2138792
12	223.2	16.5	896	29	CNS03BQM
13	222.8	16.5	736	13	BU468891
14	218.4	16.1	570	14	CD552519
15	218.4	16.1	855	29	GCAR22AR
16	211	15.6	966	29	CNS02NV2
17	205.8	15.2	893	12	BI459381
18	205.4	15.2	415	9	AW785035
19	198.6	14.7	805	29	CNS03CEB
20	184.4	13.6	801	29	GCAR22AR
21	183.2	13.5	863	14	CD361190
22	182.2	13.5	1201	9	AL573897
23	178.8	13.2	774	29	AGAA202AR
24	175.8	13.0	819	29	CCAA22AR
25	175	12.9	1176	9	AL549866
26	174.6	12.9	619	10	AW16723
27	172.8	12.8	1201	9	AL54577
28	167.6	12.4	777	29	LRBA22AR
29	164.4	12.2	555	9	AL588968
30	161.8	12.0	301	14	T39448
31	159.8	11.8	753	29	SCAA22AR
32	158.8	11.7	575	13	BU377890
33	158.4	11.7	767	13	BU376517
34	157.4	11.6	451	9	AI461341
35	156.8	11.6	1010	29	CNS04CMQ
36	155.6	11.5	1201	9	AL530417
37	155.4	11.5	859	14	CD360383
38	155.4	11.5	920	14	CD360119
39	155.2	11.5	882	29	HIPAC22AR
40	154.8	11.4	825	29	ARUA22AR
41	154.6	11.4	1080	29	CC240340
42	154.4	11.4	890	29	CNS02WKR
43	153.8	11.4	911	14	CD360520
44	153.2	11.3	974	29	PTRA22AR
45	153	11.3	926	29	CNS012C8

ALIGNMENTS

RESULT 1
ECAA2BAR
LOCUS
DEFINITION
Horse alpha2 adrenergic receptor gene fragment probably subtype b,
genomic survey sequence.

ACCESSION
AL606560
VERSION
AL606560.1 GI:15591917
KEYWORDS
GSS; Alpha2 adrenergic receptor gene.
SOURCE
Equis caballus (horse)
ORGANISM
Equis caballus

REFERENCE
1 (bases 1 to 872)
AUTHORS
Hunter, C. and Elgar, G.
TITLE
Alpha2 adrenergic receptor gene
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 872)
AUTHORS
Hunter, C.
TITLE
Direct Submision
JOURNAL
Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hmp.mrc.ac.uk

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9796"

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Query Match	48.4%;	Score 654.4;	DB 29;	Length 872;
Best Local Similarity	87.0%;	Pred. No. 2.2e-116;		
Matches 760;	Conservative	0;	Mismatches 96;	Indels 18; Gaps 3;
QY	310	TGCGGCATCAGCTGGAACGGCTAATCGGGCCGAGAGCCGCGCTGAGATCAATCCGAG	369	
DB	1	TGCCCCATCAAGCCTTGAGCGCTACTGAGCGCGGTGAGCGCGCGCTGAGATCAACACCAAG	60	
QY	370	CGACACCCGCGCGCATCAATGTCATCTCTCATCTGTGTGGCTCATCGCGCGATC	429	
DB	61	CGACACCCGCGCGCATCAATGTCATCTCTCATCGGTGTGTGTATCTGATATCGACGTGTATC	120	
QY	420	TGCGTCCGCGCGCTCATCTCAAGGGCGACCAAGGGCCCGACAGCGCGCGCGCGCCAG	489	
DB	121	TGCGTCCGCGCGCTCATCTCAAGGGCGACCAAGGGCCCGACAGCGCGCGCGCGCGCCAG	180	
QY	490	TGCAAGCTCAACAGAGAGCGCTGGTATCATCTGAGCTTCCAGATGGATCTTTCTTTGCT	549	
DB	181	TGCAAGCTCAACAGAGAGCGCTGGTATCATCTGAGCTTCCAGATGGATCTTTCTTTGCA	240	
QY	550	CCCTGCTCATCATGATCTCTTGTCTTACCTGGGATCTACCTGATGCGCAACGACGAC	609	
DB	241	CCCTGCTCATCATGATCTCTTGTCTTACCTGGGATCTACCTGATGCGCAACGACGAC	300	
QY	610	CCGAGAGGCTCCAGAGGCGCAAGAGGAGGCGCTGGCGAGGTGATCTCAAGAGCGCCGAG	669	
DB	301	CTCAGAGGCTCCAGAGGCGCAAGAGGCGCTGGCGAGGTGATCTCAAGAGCGCCGAG	360	
QY	670	GACCATGATGAGGCTTTTGCTCTGAGCCCAATGCGACGCGCTGAGCTC--TGTGCTTCT	726	
DB	361	GTCCTGCGAGAGCTTCAAGCTCAGCTCAGCCCAATGCGCTGAGCTTGTGTGAGTGTCT	420	
QY	727	GCCAGAGAGTCAACGGAACATCGAAGTCTCACTGGGAGGAAGAGAGAGGAGACCTCT	786	
DB	421	GCCGAGAGGCTCAATGGAACATCTCGAGGCCCATGGGAGAG--AGGAGGAGAGACCTCT	477	
QY	787	GAGATCTAGTGGACCCGAGCTTTGCCATCCAGTTGGCGTGGCCCTTCCCACTCAGGCCAG	846	
DB	478	GAAATCTTCTGGAGCCCTGCTGTGGCCCGCCAGCTGGCTGCTTCTTCACTTGAAGCCAG	537	
QY	847	GGCCAAGAGAGGTGTGTGTGGGAGCATCTCGAGAGATGAAGCT-----GAA	894	
DB	538	GATCAGAGAGAGAGATTTGTGGGAGATCTCTGAGAGAGGAAGCTGAAGAGAGAGAA	597	
QY	895	GAG	954	
DB	558	GAG	657	
QY	955	CCGAGCTTACGTTGACACCCCGCGCGAGCAGCAGCAGAGGCTCCCGGGTCTGGCAAC	1014	
DB	658	CCGAGCTTACGTTGACACCCCGCGCGAGCAGCAGCAGAGGCTCCCGGGTCTGGCAAC	717	
QY	1015	CTAAGTGCACAGTGTCTCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1074	
DB	718	CTAAGTGCACAGTGTCTCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	777	
QY	1075	CGAAGGCGCAGCTTACCCCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1134	
DB	778	CGGCGGCGCAGCTTACCTCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	837	
QY	1135	GTTTTGTGCTCTGCTGAGTTCCCTCTTCTTCA	1168	
DB	838	GTCTTGTGCTCTGCTGAGTTCCCTCTTCTTCA	871	
RESULT 2				
BO880026		1044 bp	mRNA	linear
LOCUS	BO880026			
DEFINITION	AGENCOURT 811358 Lupsk dorsal root ganglion Homo sapiens cDNA			
	clone IMAGE:6179035 5', mRNA sequence.			

ACCESSION	B0880026
VERSION	B0880026.1
GI:	22272034
KEYWORDS	RST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 1044)
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: gcgabs-remail.nih.gov Tissue Procurement: Dr. James R. Lupski CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1359 row: 1 column: 20 High quality sequence stop: 430. Location/Qualifiers
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	/db_xref="taxon:9606"
	/clone="IMAGE:6179035"
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	/dev_stage="adult, 36 yr"
	/lab_host="DH10B"
	/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: /clone_lib="Lupski_dorsal root ganglion" NotI; Site_2: SalI; CDNA made by oligo-dT priming. directionally cloned using the following adaptors: 5'-GACTAGTTTATGATCGCAGCGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."
BASE COUNT	182 a 334 c 345 g 183 t
ORIGIN	
Query Match	37.9%; Score 513.2; DB 13; Length 1044;
Best Local Similarity	93.5%; Prod. No. 4.3e-89;
Matches	606; Conservative 0; Mismatches 23; Indels 19; Gaps 6
Dy	464 GCCCCAGCCGCGGGCGCCCCAGTCGAAGTCGAACGAGAAGCGCTGTGCAATCTGG 523
Dy	1 GCCCCAGCCGCGGGCGCCCCAGTCGAAGTCGAACGAGAAGCGCTGTGCAATCTGG 60
Dy	524 CTTGAGATGAGATCTTTCTTGCTCTGCTCATCATGATCTTGTCTAATCTGGCA 583
Dy	61 CCTCAGATGAGATCTTTCTTGCTCTGCTCATCATGATCTTGTCTAATCTGGCA 120
Dy	584 TTTACTGATGCGCCAAAGCAGCAACCGCAGAGTCCCAGAGGCGAGGGGGGCTGGG 643
Dy	121 TTACTGATGCGCCAAAGCAGCAACCGCAGAGTCCCAGAGGCGAGGGGGGCTGGG 180
Dy	644 AGGTGATGTCGAAGAGCGCCGACCCGACATGTGTGGGCTTTGGCTCAGCCMAACTGC 703
Dy	181 AGGTGATGTCGAAGAGCGCCGACCCGACATGTGTGGGCTTTGGCTCAGCCMAACTGC 240
Dy	704 CAGCCCTGGCTCTGTGGCTTGTGCTGCAAGAGTCACAAGCACTCGAAGTCACCTGGG 763
Dy	241 CAGCCCTGGCTCTGTGGCTTGTGCTGCAAGAGTCACAAGCACTCGAAGTCACCTGGG 300
Dy	764 AGAAGAGAGAGGAGAGACCCTGAAGATACTGGAGCCCGGCTTGGCACCCAGATTGG 82
Dy	301 AGAAGAGAGAGGAGAGACCCTGAAGATACTGGAGCCCGGCTTGGCACCCAGATTGG 36

QY 824 CTGCCCCCTCCCACTGAGGCGCAGAGAGGGGTGTTTGTGGGGCATCTCCAGAG 883
 DB 361 CTGCCCCCTCCCACTGAGGCGCAGAGAGGGGTGTTTGTGGGGCATCTCCAGAG 420
 QY 884 ATGAGCTGAG 943
 DB 421 ATGAGCTGAG 472
 QY 944 TGGCAATGCTCTCCGGGCTTCAAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAG 1001
 DB 473 TGGCAATGCTCTCCGGGCTTCAAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAG 532
 QY 1002 GGTGGTGGGCGACCC--TAGCTGCGAGAGTCTCC--TGGGAGAGAGAGAGAGAG 1056
 DB 533 GGTGGTGGGCGACCCCTTCAAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 592
 QY 1057 GGTGGTGGGCGAGTGTGGGCTCG---AAGGGCGAGAGTGAACCCGGAGAGAA 1100
 DB 593 AGTGGGAGAGAGTGTGGGCTCGAAGCGGGCGAGAGTGAACCCGGAGAGAA 640

RESULT 3
 BC035047
 LOCUS
 DEFINITION Homo sapiens, similar to adrenergic, alpha-2A-, receptor, clone
 IMAGE:5266354, mRNA.
 ACCESSION BC035047
 VERSION BC035047.1 GI:23272892
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadany@systemsbio.org
 Anup Madan, Jeessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAX Plate: 73 Row: 0 Column: 16
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 15718669
 This clone has the following problem: frame shifted.

FEATURES

SOURCE
 1. 2410
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 /clone="IMAGE:5266354"
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 /note="Vector: pBluescript"
 BASE COUNT 406 a 813 c 721 g 470 t

Query Match 32.7%; Score 442.4; DB 11; Length 2410;
 Best Local Similarity 62.8%; Pred. No. 2.4e-75;
 Matches 846; Conservative 0; Mismatches 421; Indels 81; Gaps 7;

QY 15 CCCCTACTCCGTCAGAGCCACAGCGGCATAGCGGGCGGCATCACTTCTCTCTCT 74
 DB 291 CCTTATCTCCCTGACAGTACAGCTGAGCTGTGTCCTGGCCGCTCTCACTGTCT 350
 QY 75 TACCATCTTCCGAGAGCTCTGAGTATCCGCTGCTGTGACAGCGCTCTGCGCC 134
 DB 351 CACCTGTTCCGAGAGCTGTCTGTCTATCTGCTGCTGCTGCTGCTGCTGCTGCT 410
 QY 135 CCCTGAGAACCTGTTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
 DB 411 GCCCAAAACCTTCTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
 QY 195 CATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
 DB 471 CATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
 QY 255 CGAGGTGTAACCTGAGCTGAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 314
 DB 531 CGAGATCTTACCTGAGCTGAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 590
 QY 315 CATCACTCTGAGCCGCTACTGAGCGCTGAGCGCGCTGAGTACACTTCAAGCGCAC 374
 DB 591 CATCACTCTGAGCCGCTACTGAGCGCTGAGCGCGCTGAGTACACTTCAAGCGCAC 650
 QY 375 CCGCGCGCGCATCAAGTGCATCTCTCACTGTGTGCTTCATGCGCGCTCATCTGCT 434
 DB 651 GCCGCGCGCATCAAGTGCATCTCTCACTGTGTGCTTCATGCGCGCTCATCTGCT 710
 QY 435 GCCGCGCGCTCATCT-----ACAAAGGCGACAGAGCGCCCGACCGCGCGCGCC 485
 DB 711 CCGCGCGCTCATCTCTCATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 770
 QY 486 CCACTGAGAGCTCAACAGAGAGCGCTGTATCATCTGAGCTCTGAGATCGGATCTTCT 545
 DB 771 GCGCTGAGAGTACAGACAGAGAGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCT 830
 QY 546 TGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
 DB 831 CCGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
 QY 606 CAACCGCAGAGTCCCAAGAGCGCCAAAGGGGGGCTGGGAGAGTTCAGAGAGCCCG 665
 DB 891 CAACCGCAGAGTCCCAAGAGCGCCAAAGGGGGGCTGGGAGAGTTCAGAGAGCCCG 931
 QY 666 ACCGAGCATGTGTGGGCTTTGAGCTTCAAGCAAGCTGAGCGCTGCTGCTGCTGCT 725
 DB 932 CCG 973
 QY 726 TGCAGAGAGTTCACAGACCTTCAAGTCTGAGAGAGAGAGAGAGAGAGAGAGAG 785
 DB 974 GCCCGAG 1026
 QY 786 TGAAGATCTGAG 845
 DB 1027 CAGCTCAAG 1086
 QY 846 GGGCGAG 905
 DB 1087 GACCTGAG 1146
 QY 906 GAG 965
 DB 1147 GAGCGGAG 1206
 QY 966 TTGAG 1025
 DB 1207 CTGCG 1251
 QY 1026 GGTGCTCTGAG 1085

Accession	Sequence	Position
Db	1232 GCAGGCGCGGGGGAGAGCGCGTCGG-----GGCTGCCAAGGCGTTCGCGCTGGCGCGGGCG	1307
Qy	1086 GCTGACCCGGGAGAAAGCGCTTCACCTTCGTGTGGCTGTGTCATTGGCGTTTGTGCT	1145
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Qy	1146 CTGCTGTTTCCCTCTTCCTTCAGGTACAGCGTGGGCGGCATCTGAGCCGGAAGCACTGAA	1205
Db	1368 GTGCTGTTCCCTCTTCCTTCACCTTACAGCTACAGGCGCGTGG-----GTGCTC	1418
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Qy	1326 CGGCGCGTGAAGCCAGACGAGCGCTGGTGA	1353
Db	1539 TCGGGGGACACAGAACCGGATCTGTGTA	1566

RESULT 4	
AK046802	
LOCUS	AK046802
DEFINITION	Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN
	3584 bp mRNA linear HTC 05-DEC-2002

ACCESSION	AK046802
VERSION	AK046802.1 GI:26091726
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED
1	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	Meth. Enzymol. 303, 19-44 (1999)	992796253	
2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				10349636

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillarary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCES	4
AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,

Kawai, J., Shingawara, A., Shibata, K., Yoshino, M., Itoh, M., Ishiy, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Aoechi, Y., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsumura, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Glisic, C., King, B., Kouchiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.

Quackenbush, J., Schirral, L.M., Scabelli, F., Suzuki, R., Tomita, M., Wagner, L., Mashio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barash, G., Blake, J., Boffelli, D., Bojunga, N., Cincinelli, P., de Bernaldo, M.F., Brownstein, M.J., Bul, C.C., Fletcher, C., Fujita, M., Gariboldi, M., Guscinich, S., Hill, D., Hochmann, M., Hume, D.A., Kaniya, M., Lee, N.H., Lyons, P., Marchionni, L., Maehama, J., Mazzarelli, J.J., Mommaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Saeki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilting, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohseuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

JOURNAL MEDLINE
PUBMED 21085660
11217851

REFERENCE
5

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

The PANTOM Consortium and the RIKEN Genome Exploration Research

JOURNAL
REFERENCE
AUTHORS
Nature 420, 563-573 (2002)
6 (bases 1 to 3594)
Adachi, J., Atawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Hasegawa, K., Hayatsu, N., Hamoto, A., Hiraga, I., Hirobae, Y., Hori, F., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukabe, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kuliwara, K., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Oshato, N., Ozakaki, Y., Saito, K., Saitoh, H., Sakai, K., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takano-Akahira, S., Ikeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

JOURNAL
Submitted (16-JUL-2001) Yoshihide Hayashiraki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://tancom.gsc.riken.go.jp/>.

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3594
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BASE COUNT 691 a 1117 c 1019 g 767 t
ORIGIN

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Query Match 28.9%; Score 390.6; DB 11; Length 3594;
 Best Local Similarity 60.8%; Pred. No. 2,7e-65;
 Matches 804; Conservative 0; Mismatches 439; Indels 80; Gaps 7;

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 Db CCCCTACTCCGTGAGGCGCAGAGGCGCATAGCGCGCCCATACCTTCTCATTTCTT 1009

950 CCCCTACTCCGTGAGGCGCAGAGGCGCATAGCGCGCCCATACCTTCTCATTTCTT 1009

75 TACCATTTGGGAGGCGCTGCTGATCTGAGCTGTGATGACAGCGCGCTGCGCGCGC 134
 Db CACAGTATTGGGAGGCGCTGCTGATTTATGCGGCTGTACAGAGCGCGCTCAAGC 1069

1010 CACAGTATTGGGAGGCGCTGCTGATTTATGCGGCTGTACAGAGCGCGCTCAAGC 1069

135 CCCCTAGAACTGTCTGCTGTGCTGCTGCGCGCGCGCATCTGCTGAGCAAGCTCAT 194
 Db TCCCAAAACCTCTCTGCTGTGCTGCTGCGCGCGCATCTGCTGAGCAAGCTCAT 1129

1070 TCCCAAAACCTCTCTGCTGTGCTGCTGCGCGCGCATCTGCTGAGCAAGCTCAT 1129

195 CATCCCTTTCTGCTGCGCGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
 Db CATTCCTTTCTTGTGCGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189

255 CGAGGTGTACCTGCGCGCTGAGCGCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 314
 Db TGAATCTATTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1249

1190 TGAATCTATTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1249

315 CATGAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 374
 Db CATGAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1309

1250 CATGAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1309

375 CCGCGCGCGCATGAGTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
 Db GCGCGCGCGCATGAGTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1369

1310 GCGCGCGCGCATGAGTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1369

435 GCGCGCGCGCATCT-----ACAGGCGCGAGCAGAGGCGCGCGCGCGCGCGCG 485

1370 CCGCGCGCATCTCTCTCATAGAGAGAGAGGCGCGCGCGCGCGCGCGCGCGCG 1429

486 CAGTGCAGCTGAGCGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545

1430 AACTGCAAGTACAGAGCAGAGAGAGTGTATCTCTCTGCTGCTGCTGCTGCTGCT 1489

546 TGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605

1490 CCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549

606 CAGCGCGAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 665

1550 CAGCGCGAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1603

666 ACCGAGCATGAGGCGCGCTTGGCGCTGAGCAAGTGCAGCGCGCGCTGCTGCTG 725

1604 GCGCGCGCATGCGAG-----CCAGAGCGCGCTGCGCGCGCGCGCGCGCGCG 1651

726 TGCAGAGAGTCAACGAGCATCTGAGTCACTGCGAGAGAGAGAGAGAGAGAGAG 785

1652 TCCCAAGGCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1711

786 TGAAGTACTGGAGAGCGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 845

1712 CG-----CGCGCGCGCGCGCGCGCGCGCGCGAGTGGAGAGCGCTGAGAGG 1759

846 GCGCGAG 905

1760 -----GTTGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1806

906 GAG 965

1807 GACCGGCGCGCGAG 1866

966 TTGAGAGCG 1025

1867 CTGCG 1907

Qy 1026 GTGCTCTGCGAGGCGCTGAGTGTCTATAGTGTGAGCGAGTGTGCGTGAAGGCGCA 1085
 Db GGGGTCCGGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1967

Qy 1086 GCTGAGCGCGGAG 1145
 Db GCAAAACCGGAG 2027

1146 CTGCTGAGTCCCGCTCTCTCTGAGCTACAGCTGAGGAGCGCATGCGCGAGAGAGCA 1205
 Db GTGTGAGTTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2078

2028 GTGTGAGTTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2078

Qy 1206 GTGCGCGAGAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1265
 Db GTGTGCGAGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2138

2079 GTGTGCGAGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2138

Qy 1266 CCGTGTATTTACACATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1325
 Db CCGTGTATTTACACATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2198

2139 CCGTGTATTTACACATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2198

Qy 1326 CCG 1328
 Db 2199 CCG 2201

RESULT 5
 AL544609
 LOCUS
 DEFINITION
 AL544609 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1021YC24 5-PRIME, mRNA sequence.
 AL544609
 VERSION
 AL544609.2 GI:31266452
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 1201)
 AUTHORS
 Li W.B., Gruber, C., Jessee, J. and Polyes, D.
 TITLE
 Full-length cDNA libraries and normalization
 JOURNAL
 Unpublished
 COMMENT
 On Feb 15, 2001 this sequence version replaced gi:12877089.
 CONTACT
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5594.f. For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1021B120P1&cluster=5594.f. Contact :
 Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0D1021B120P1.

FEATURES

source
 1. 1201
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 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT
 155 a 430 c 425 g 184 t 7 others

Query Match 23.9%; Score 324; DB 9; Length 1201;
 Best Local Similarity 74.8%; Pred. No. 1.5e-52;
 Matches 446; Conservative 0; Mismatches 145; Indels 5; Gaps 3;

RESULT 7
 BQ887729 988 bp mRNA linear EST 16-AUG-2002
 LOCUS BQ887729
 DEFINITION AGENCOURT 8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
 5' mRNA sequence.
 ACCESSION BQ887729
 VERSION BQ887729.1 GI:22279743
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 988)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@ds-r@mail.nih.gov
 Tissue Procurement: Susan L. Sullivan, PhD.
 CDNA Library Preparation: Resgen, Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLAM3739 row: m column: 06
 High quality sequence start: 8
 High quality sequence stop: 509.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:10090"
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 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_129"
 /note="Organ: olfactory epithelium; Vector:
 pCMV-SPORT6.1.cdb; Site 1: EcoRV; Site 2: NotI; Cloned
 unidirectionally. Primer: Oligo dT. Average insert size
 2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this
 is a NIH MGC Library."
 18 a NIH MGC Library."
 BASE COUNT 158 a 349 c 300 g 181 t
 ORIGIN
 Query Match 21.8%; Score 295.4; DB 13; Length 988;
 Best Local Similarity 76.4%; Pred. No. 4.9e-47;
 Matches 389; Conservative 0; Mismatches 116; Indels 4; Gaps 2;
 106 GCTGTGTGACACGCGCTGCTGCGCGCCCTCAGAACTGTTCTGCTGCTGCGCAAGCTGCT 165
 19 GCTGTGTGACACGCGCGCTGCTGCGCGCCCTCAGAACTGTTCTGCTGCTGCTGCGC 78
 166 GCCGC-CGACATCTGCTGCGCAAGCTCATCTCTTCTGCTGCGCAAGCTGCT 224
 79 TCAGCTAACACATCTGCTGCGCAAGCTGCTGCTTCTGCTGCGCAAGCTGCT 138
 225 GGGCTACTGCTACTCTCGCGCGCAAGCTGCTGCGCAAGCTGCTGCTGCTT 284
 139 GGGCTACTGCTACTCTCGCGCGCAAGCTGCTGCTGCTGCTGCTGCTGCTT 198
 285 CTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
 199 CTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258
 345 CCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
 259 GCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
 405 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
 319 CGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 375
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RESULT 8
 BB643669/c 691 bp mRNA linear EST 26-OCT-2001
 LOCUS BB643669
 DEFINITION BB643669 RIKEN full-length enriched, adult male corpora
 quadrigenina Mus musculus cDNA clone B23052011 5', mRNA sequence.
 ACCESSION BB643669
 VERSION BB643669.1 GI:16478370
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 691)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
 Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda,
 M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Sasaki,
 Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,
 D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
 Yamamatsu, M., and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 JOURNAL Unpublished
 COMMENT Contact: Yoshinori Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,
 M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Makihi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura,
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10
 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
 Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa,
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and
 Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.
 Location/Qualifiers
 1..691
 /organism="Mus musculus"
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BASE COUNT	156	182	233	118
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Query Match	Similarity	20.6%	Score 278.4	DB 10	Length 691
Best Local	Similarity	70.8%	Pred. No. 8.7e-44		
Matches	388	Conservative	0	Mismatches 151	Indels 9
					Gaps 1
QY	15	CCCTTACTCGGTGACGACCAAGCGGCATAGCGCGGCATCATCTTCTCATTTCTT	74		
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QY	75	TACCATCTTGGGCAACGCTTGTGTATCTGTGCTGTGTGACCAAGCCCTGTGCGGCG	134		
Db	489	CACATATATTTGGCAACGCTGTGTATATGCGCGGTGTTCACAGTCCGGGCTCAAAAG	430		
QY	135	CCCTCAGAACCTGTTCTGTGTGTGCTGTGACCGCGCCGACATTCCTGTGGGCAAGCTCAT	194		
Db	429	TCCCAAAACCTCTTCTGTGTGTCTCCCTGGCTCAGCGGACATCTGTGTGGCAAGCTGT	370		
QY	195	CATCCCTTTCGCTGCGCAACGAGCTGTGGGCTACTGTATCTTCCGGCGCAAGTGGTG	254		
Db	369	CATTCCTTTTCTTGGCCAAAGAGGTATAGGGTTACTGTACTTGTGTAAAGTGTGGTG	310		
QY	255	CGAGTGTACTGTGGGCTGTGACATGTCTCTTCTGCACTCTGTTCATCTGTGACATCTGTGGC	314		
Db	309	TGAGATCTATTTGGGCTGTGACGTGTCTTTTGTGACGTGTGTCATATGACACTGTGTGGC	250		
QY	315	CATCAGCTGTGACCGCTACTGAGGCGGTGAGCGCGCTGTGAGTACACTCCAAGCGCAC	374		
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QY	435	GCGGCGCTCATCT-----ACAAGGGGCAACGAGGGCCCCCAGCGCGCGGCGCGCC	485		
Db	129	CCCGGCATCTATCTCATAGAGAAAGAGGCGCTGCGCGCGGCGAGCGCGCGGAGCC	70		
QY	486	CCAGTGAAGCTCAACGACGAGGCGCTGTGTAATCTGTGCTTCAGACATCGATCTTTCTT	545		
Db	69	AAGCTGCAAGATCAACGACGACAGAGGTGTATGTATCTCTCTGTTCATCGGTTCTTCTT	10		
QY	546	TGCTCTT 553			
Db	9	CGCGCTT 2			

LOCUS	AC0046211/c
DEFINITION	2736 bp mRNA linear HTC 05-DEC-2002
ACCESSION	AK046211
VERSION	AK046211.1 GI:26091387
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci, P. and Hayashizaki, Y.
AUTHORS	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE	Itoh, M., Komu, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to
PUBMED	prepare full-length cDNA libraries for rapid discovery of new genes
GENOME	Genome Res. 10 (10), 1617-1650 (2000)
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P.,

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 2736)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagata, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadote, K., Matsuda, H., Ashburner, M., Batilov, S., Cavaletto, F., Fleischmann, W., Gaasterland, T., Gissi, C., Kling, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schirml, L.M., Scabelli, F., Suzuki, R., Tomita, M., Wagner, L., Mashio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., C. Hill, D., Fletcher, C., Fujita, M., Gariboldi, M., Gasciunchi, S., Hill, D., Hochmann, P., Hune, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombauts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Saeki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshak-Bois, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Konturki, S., and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 11217851

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

Location/Qualifiers

1. 2736

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/mol_type="mRNA"

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/db_xref="taxon:10090"

/clone="B230352011"

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/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

1. 2736

/note="unknown EST (GB|BB633673, evidence: BLASTN, 100%, match=279)"

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ORIGIN

Query Match 20.6%; Score 278.4; DB 11; Length 2736;

Best Local Similarity 70.8%; Pred. No. 1.2e-43;

Matches 388; Conservative 0; Mismatches 151; Indels 9; Gaps 1;

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549 CCCTTACTCCGTCAGGTCAGTCAGCGCTGTTGCTGCGCTGCTCATGCTGTT 490

75 TACCATCTTGGCAAGCGCTGTGTCATCTGCTGTGTGTAACCAAGCCGCTGCGCGC 134

489 CACAGATTTGGCAAGCGCTGTGTTATATATCGCGGTGTTACCAAGTCGCGCTCAAGC 430

135 CCTCAGAACCTGCTGCTGTGTCGTCGCGCGCCGCGCATCTGTCGCGCAAGCTCAT 134

429 TCCCAAAACCTCTTCTGCTGTGTCGTCGCGCTCAAGCGAATCTGTGCGCAGCTGCT 370

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369 CATTCCTTTCTTGGCGCAAGAGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAG 310

309 TGAGATCTATTGGCTCTGACGTCGCTTTTGACGTCGTCATAGTGAACCTGTGCGC 250

255 CGAGGTGATCTGCGCTGACGTCGCTTTTCTGACCTGTCATGTCGTCGTCGTCGTC 314

315 CATCAGCTTGGCAAGCGCTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 374

249 CATCAGCTTGGCAAGCGCTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 190

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Db 189 GCCGCTGCATCAAGGCGCATATGTCACGTCGTGGTCTCTGCTGTCATCTTCTT 130

435 GCCGCCCTCATCT-----ACAAGGCGACAGAGCCCGCCAGCGCGCGCGCC 485

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69 AACCTCAAGATCAAGACAGAGAGGTCATCTCTGTCATGCTGCTTCTTCTTCTT 10

546 TGCTCTCTT 553

9 CGGCGCTT 2

RESULT 10

CA477609

LOCUS

DEFINITION

AGENCOURT 10671423 NCI CGAP Zemb3 Danio rerio cDNA clone

CA477609

IMAGE:6801483 5', mRNA sequence.

CA477609.1 GI:24933961

EST.

Danio rerio (zebrafish)

Danio rerio

ACTINOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Cyprinidae; Danio.

1 (bases 1 to 909)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgap@remail.nih.gov

Tissue Procurement: Dr. Chi-Bin Chien

cDNA Library Preparation: Invitrogen Corp

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

plate: L14M14321 row: e column: 02

High quality sequence start: 17

High quality sequence stop: 644.

Location/Qualifiers

1. 909

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:6801483"

/tissue_type="embryo"

/lab_host="DH10B (T1-resistant)"

/note="Vector: PCMV-SPORE.ccd; Site 1: EcoRV; Site 2:

NotI; Cloned unidirectionally. Primer: Oligo dt. Average

insert size 2.1 kb. Constructed by J. Wang (Research

Genetics, Invitrogen Corp) from tissue donated by L. Zon

(Harvard University). Note: this is a NCI CGAP Library."

BASE COUNT 156 a 287 c 266 g 200 t

ORIGIN

Query Match 19.7%; Score 267.2; DB 14; Length 909;

Best Local Similarity 76.2%; Pred. No. 1.3e-41;

Matches 329; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

16 CCTACTCGTGAGCGCAAGAGCGCATAGCGCGGCATCACTTCTCATTTCTTCTT 75

306 CCTTACCGAGCGCGCTTCCGATCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 365

76 ACCATTTGGCAAGCGCTGTGTCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 135

366 ACTATGTCGGAATATTTCTTGTGATGTCGTCGCTTTTGAACGAGCGCGCTGCGCT 425

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QY 136 CCGAGAGAGCTGTTCCGATGATGCTGGCCGCGGACATCTGATGAGCCAGCTCATC 195
 DB 426 CCGAGAGAGCTGTTCCGATGATGCTGGCCGCGGACATCTGATGAGCCAGCTCATC 485
 QY 196 ATCCCTTTCTCGTGGCCCAAGAGCTGCTGGGCTACTGTAATTCGGCCGACGTGTGC 255
 DB 486 ATCCGCTTCTCCCTCGCCCAAGAGATCATGGATATGTAATTCGGCCGACCTGTGTGC 545
 QY 256 GAGGTGATCTGGGCTGACAGCTGCTTCTTGTGACCTTCGTCATTCGGGACCTGTGTGC 315
 DB 546 GCGTTTACCTGGGCTGAGATGCTGCTTCTTGTGACCTTCGTCATTCGGGACCTGTGTGC 605
 QY 316 ATCAGCTTGAGCGCTACTGGGCGCTGAGCCGCGCGCTGAGATCACTCAAGCGCAC 375
 DB 606 ATCAGCTTGAGCGCTACTGGTCCGTCACCAAGCGGTGCGCTCAACCTGAAGCGCAC 665
 QY 376 CCGGCGCGCATCAAGTGCATCATCTGATCTGTGTGCTCATTCGCGCGCTCATCTGC 435
 DB 666 CCGAGGCGCATCAAGTGCATCATCTGCGGCGGTGTGTGTGATCTCCGCGCTCATCTGC 725
 QY 436 CCGCGCTCATC 447
 DB 726 CCGCGCTCATC 737

RESULT 11 677 bp DNA linear GSS 11-OCT-2002
 BZ138792/c
 LOCUS CH230-256D20.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
 DEFINITION CH230-256D20, genomic survey sequence.
 ACCESSION BZ138792
 VERSION BZ138792.1 GI:23779739
 KEYWORDS GSS.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 677)
 Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
 'A., Gebreyesgeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
 Jong,P. and Frazer,C.M.
 Rat BAC End Sequences from Library CHORI-230 MboI segment
 Unpublished
 Other_GSSs: CH230-256D20.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@igf.org
 Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.html). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or_ering_information.htm). BAC end
 plate: http://www.igf.org/cdb/bac_ends/rat/bac_end_intro.html
 Seq primer: 77
 Class: BAC ends.

FEATURES

Source
 1. 677
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="BN/SsNHed/MCM"
 /db_xref="taxon:10116"
 /clone="CH230-256D20"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 2"
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 CHORI-230 Rat (BN/SsNHed/MCM) BAC library produced by

BASE COUNT 139 a 200 c 220 g 118 t
 ORIGIN

Query Match 19.4%; Score 262.6; DB 28; Length 677;
 Best Local Similarity 74.4%; Pred. No. 9,7e-41;
 Matches 331; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 23 CCGTGAAGCCACAGAGCGGCGCATAGCGGCGCATCACTTCTCATATCTTACCATCT 82
 DB 502 CCTGAGAGTGAAGCTGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 443
 QY 83 TCGGCAAGCGCTGT 142
 DB 442 TTGGCAAGCGCTGT 383
 QY 143 ACCTGTCTGT 202
 DB 382 ACCTGTCTGT 323
 QY 203 TCTGT 262
 DB 322 TTCTGT 263
 QY 263 ACCTGT 322
 DB 262 ACTGT 203
 QY 323 TGGACCGCTGT 382
 DB 202 TTGACCGCTGT 143
 QY 383 GCATCAAGTGCATCATCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 442
 DB 142 GCATCAAGGCGCATATGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 83
 QY 443 TCATCTACAAGGCGGACGAGGCGC 467
 DB 82 TCATCTCAATAGAGAGAGGCGC 58

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

RESULT 12 896 bp DNA linear GSS 01-SEP-2000
 LOCUS CNS03BQW
 DEFINITION Tetradon nigroviridis genome survey sequence PUC-ori end of clone
 012P03 of library G from Tetradon nigroviridis, genomic survey
 sequence.
 ACCESSION AL236849.1 GI:7895984
 VERSION AL236849.1
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetradon nigroviridis
 ORGANISM Tetradon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

1 Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 Estimate of human gene number provided by genome-wide analysis
 using Tetradon nigroviridis DNA sequence
 Nat. Genet. 25 (2), 235-238 (2000)
 MEDLINE 20296633
 PUBMED 10835645

2 Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C.,
 Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
 Saurin,W., Bernot,A. and Weissenbach,J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetradon nigroviridis
 Genome Res. 10 (7), 939-949 (2000)
 MEDLINE 20359837

REFERENCE	PUBMED	10899143
AUTHORS	3	(bases 1 to 896)
TITLE	Genoscope.	
JOURNAL	Direct Submission	
COMMENT	<p>This sequence is a single read and was generated as part of a large-scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon.</p>	
FEATURES	source	1..896
	<p>location/Qualifiers</p> <p>1..896</p> <p>/organism="Tetraodon nigroviridis"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:99883"</p> <p>/clone="012P03"</p> <p>/clone_11b="G"</p> <p>/note="Genoscope sequence ID : C0B6012CH02SP1-end : PUC-Or1"</p>	
BASE COUNT	163 a	276 c 295 g 157 t 5 others
ORIGIN		
Query March	16.5%	Score 223.2; DB 29; Length 896;
Best Local Similarity	73.8%	Pred. No. 4.2e-33;
Matches	282; Conservative	1; Mismatches 99; Indels 0; Gaps 0;
QY	9 CCAGGACCCTTACTCCGTGCAAGGCCACAGCGGCATACCGGCGGCATACCTTCCTCAT 68	
DB	488 CTTGAGCGGCTACTCTCTTAAGGGGCCACGGCGGCATGCGCGCTCGTCAAGCTTCTCAT 547	
QY	69 TCTCTTACCATCTTGGGCAAGCCTCTGTGATCTGCTGTGTTGACAGCGCTGCT 128	
DB	548 CTTGTTCACGGTGTGCGGAAATCTCTGTGTGTCTCCGGTGTGAGAACCGGCGCT 607	
QY	129 GCGGCGCCCTCAGAACCTGTCCTGTGCTGTGCTGTGCGCGCGCCGACATCTGTGGCCAC 188	
DB	608 CAGAGCGCGGAGAACCTTCTCTGTGTGTCTGTGACCGGAGACATCTGTGTGCGAC 667	
QY	189 GCTCATATCCCTTCTTCTGCTGCGCCAGAGCTGCTGAGCTTACTGTCTTCCGCGCAC 248	
DB	668 CTTGTGATGCTCTTCTCTGCGCCAGACTGATGGGCTTACTGTATTTTCGAGAGGT 727	
QY	249 GTGTGTGAGGTGTACTGGCGCTCGACGTGCTCTTGTGCACTCTGTGCATGTGACCT 308	
DB	728 CTGTGTGCGGAGTTTATCTGTGCTGTGATGTTTATTTATTTGTGCACTGTGTGATCT 787	
QY	309 GTGCGGCATACGCTTGAACCGCTATATGGGCGGTAGCCGCGCTGAGATCACTCCA 368	
DB	788 GTGCGCATATTAAGCTTGAACCGCTATCTGTGTGTCACGAGCGGTTCAGTCAACTGAA 847	
QY	369 GCGCACCCCGCGCGCATCAAG 390	
DB	848 GAGGACCCCTCAGCGCGTMAAG 869	
RESULT 13		
LOCUS	BU468891	736 bp mRNA linear EST 30-NOV-2002
DEFINITION	603365259P1 CSEQRBN21 Gallus gallus CDNA clone CHEST72631e 5', mRNA	
ACCESSION	BU468891	
VERSION	BU468891.1	
KEYWORDS	EST.	
SOURCE	Gallus gallus (chicken)	
ORGANISM	Gallus gallus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	
REFERENCE	Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Butt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A., and Hubbard, S.J.	
AUTHORS	A Comprehensive Collection of Chicken cDNAs	
TITLE		

JOURNAL
MEDLINE
PUBMED
12445392

COMMENT
Curt. Biol. 12 (22), 1965-1969 (2002)
22335534
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)

FEATURES
source
Location/Qualifiers
1..736
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST763e16"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="CSEORBN21"
/note="Organ: ovary; Vector: Bluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntend, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT
150 a 214 c 192 g 180 t
ORIGIN

Query Match 16.5%; Score 222.8; DB 13; Length 736;
Best Local Similarity 71.8%; Pred. No. 4.8e-33;
Matches 306; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

OY 188 CGCTCATTCCTCTTTCGCTGSCCAAGAGCTGTGGCTACTGTAATCTTCGCGCGCA 247
Db 4 CTCTGTTATGCTTTCTCTTCTTGSCCAAGAGCTGATGAATCACTGTAATCTTGGCAAG 63
OY 248 CGTGTCGAGAGTATCTTCTGCGCTGCACGTGCTCTTCTGCACTCGTCAATCGTGAAC 307
Db 64 TGTGTGTCAACATCTTACCTGCGCGGTGATGTGCTCTTCTGCACTCTCCATCTTCAC 123
OY 308 TGTGCGCATCAGGCTGAGACGCTACGTCGAGGCGCGGCGCGCTGAGTACAATCTCA 367
Db 124 TGTGTGCATCAGCTTGCACAGATATGTTGTGTGCTGACGACAGGCGGTGAGTAACTCA 183
OY 368 AGCGACACCGCGCGCGCATCAAGTCAATCTCTACTGTGTGTGCTCATCGCGCGCTCA 427
Db 184 AGCGACACCTCGCGCGCATCAAGGCAATGTGCACTGTCTGCTGCTATTTCTGCTGTA 243
OY 428 TCTGTGCTGCGCGCTCTATCTACAGGCGCACAGGCGCGCGCGCGCGCGCGCGCG 487
Db 244 TTTCTCTTTCGCGCGCTTATCTTCACATG---TACCGGAGCCTTGGAAGAGATGCTTTTCCC 300
OY 488 AGTCAAGCTCAACAGAGGCGCTGATCAATCTCGGCGCTCAGCATCGAATCTTTCTTTG 547
Db 301 AGTCAAGCTCAAGAGAGACATGATCAATCTTTCTTCTGATGTTCTCTTTCTTTG 360
OY 548 CTCCTTGCCTCATCATGATCTTGTCTTACCTGCGCATCTACCTGATCGCAAGCAGCA 607
Db 361 CACCTTGCCTCATCATGATGTTGTGTATATCCGTAATCAACGTTGGCCAAAGTAAGA 420
OY 608 ACCGCA 613

Db 421 CCAGGA 426

RESULT 14
CD552619 570 bp mRNA linear EST 11-JUN-2003

LOCUS B0346C06-5 NIA Mouse E9.5 whole Embryo cDNA library (long) Mus

DEFINITION Musculus cDNA clone NIA:B0346C06 IMAGE:30433469 5', mRNA sequence.

ACCESSION CD552619

VERSION CD552619.1 GI:31600350

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE B0346C06-5 NIA Mouse E9.5 whole Embryo cDNA library (long) Mus

AUTHORS Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.

TITLE Construction of long-transcript enriched cDNA libraries from

submicrogram amounts of total RNAs by a universal PCR amplification

METHOD Genome Res. 11 (9), 1553-1558 (2001)

JOURNAL 21429098

MEDLINE 11544199

COMMENT Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@igsun.grc.nia.nih.gov

Plate: B0346 row: C column: 06

Seq primer: M13 Reverse

High quality sequence scop: 570

POLYA=No.

Location/Qualifiers

1. 570

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="NIA:B0346C06 IMAGE:30433469"

/tissue_type="E9.5 whole embryo"

/dev_stage="whole embryo including extraembryonic tissues

at 9.5-days postcoitum"

/lab_host="DH10B"

/clone_11b="NIA Mouse E9.5 whole Embryo cDNA library (long)

")

/note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;

Site_2: NotI; Mouse cDNA project by the Laboratory of

Genetics, National Institute on Aging (NIA), Intramural

Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).

This is a long-transcript enriched cDNA library (Ref.

Genome Res. 11: 1553-1558 (2001). (PMID: 11544199). Total

RNAs were extracted from a pool of 16 embryos at 9.5-days

postcoitum. Double-stranded cDNAs were synthesized with an

Oligo(dT) primer (Invitrogen:

5'-pGACTAGTCTAGATCGGAGCGCGCCCTTTT-3')

from 6.1 ug of total RNA, treated with T4 DNA polymerase,

and purified by ethanol-precipitation. The cDNAs were

ligated to lone-linker L1-Sal4, purified by

phenol/chloroform, and separated from free linkers by

Centriclon 100. Then, the cDNAs were amplified by

long-range high fidelity PCR using Ex Taq polymerase

(Takara) with a primer Sal4-S. The products were purified

by phenol/chloroform and Centriclon 100. The cDNAs were

digested with SalI and NotI enzymes and cloned into

SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E.

coli host was transformed with the ligation mixture by the

standard chemical method. The average insert size is about

3.0kb. The library was constructed by Yulan Piao."

BASE COUNT 93 a 186 c 165 g 126 t

ORIGIN

Query Match

16.1%; Score 218.4; DB 14; Length 570;

Best Local Similarity 87.0%; Pred. No. 3.2e-32;

Matches 240; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 1 ATGACCAACCAAGACCCCTTCTCCGTCAGAGCCCAAGCGGCAATAGCGGCGCATACACC 60

Db 295 ATGATCCACCAAGAGCCCTTCTCCGTCAGAGCCCAAGCGGCAATAGCGGCGCATACACC 354

OY 61 TTCTCATCTCTTATACATCTTCCGCAAGCGCTGTGTATCTGTGTGTGTGACCAAC 120

Db 355 TTCTCATCTCTTATACATCTTCCGCAAGCGCTGTGTATCTGTGTGTGTGACCAAC 414

OY 121 CGT 180

Db 415 CGT 474

OY 181 GTGGCAGCGTCATCATCTCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240

Db 475 GTGGCAGCGTCATCATCTCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 534

OY 241 CGGCGACGTCATCATCTCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 276

Db 535 TGGCGTCGT 570

RESULT 15

GGA2AAR 855 bp DNA linear GSS 14-SEP-2001

LOCUS Chicken alpha2 adrenergic receptor gene fragment probably subtype

DEFINITION a, genomic survey sequence.

ACCESSION AL606540.1 GI:15591915

VERSION GSS; Alpha2 adrenergic receptor gene.

KEYWORDS Gallus gallus (chicken)

SOURCE Gallus gallus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 855)

AUTHORS Hunter, C. and Elgar, G.

TITLE Alpha2 adrenergic receptor gene

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 855)

AUTHORS Hunter, C.

TITLE Direct Submission

JOURNAL Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource

Centre Hinxton, Cambridge, CB10 1SB. UK Email:

biohelp@hmp.mrc.ac.uk

Location/Qualifiers

1. 855

/organism="Gallus gallus"

/mol_type="genomic DNA"

/db_xref="taxon:9031"

BASE COUNT 201 a 248 c 245 g 161 t

ORIGIN

Query Match

16.1%; Score 218.4; DB 29; Length 855;

Best Local Similarity 74.1%; Pred. No. 3.5e-32;

Matches 292; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

OY 224 TGGGCTAGTGTCTTCCGCGACAGTGTGCGAGGTGATCTGGCGCTGACGTGCTCT 283

Db 2 TGGGCTATTTGTGATCTTCCGCAAGTGTGCGAGATCTACCTGGACCTTGAGGTCTCT 61

OY 284 TCTGACCTGTCTGTCATGTGCACTGTGCGCATACCTGTGACCGGTACTGGCGGTGA 343

Db 62 TCTGACCTGTCTGTCATGTGCACTGTGCGCATACCTGTGACCGGTACTGGCGGTGA 121

OY 344 GCGCGGCTGTGATGATCACTCAAGGCAAGCGCGCGCGCATCAAGTGTGATCTCTCA 403

Db 122 CACAAGCATGATGATCACTCAAGGCAAGCGCGCGCGCATCAAGTGTGATCTCTCA 181

OY 404 CTGTGTGCTCATGTGCGCGCTGTCTGTGCGCGCGCGCATCAAGGCGCAAGG 463


```

Db      182 TCCTGGGTCATCTCGCCGTCATCTCTCCGCGCTCATCTCCATAGAGAGAGA 241
Qy      464 GCGCCGAGCCG-----CGCGGGGCGCCCGAGTGCAGCTCAACAGAGAGCGCTGTACA 517
Db      242 GTGGGCAAGCAGTGCAGCAAGTGGCGCGCAGATGCANAGATCANAGAGAGTGTACA 301
Qy      518 TCCTGGGCTTCAGCATCGATCTTTCTTTGCTCTGCTCATCATGATCTGTCTACC 577
Db      302 TCATCTGTCGAGCATCGGCTCTCTTTCACCCCGTGCTCATCATGATCTGTGTACC 361
Qy      578 TCGGCATCTTACCTGATCGCCAAAGCAGCAACCG 611
Db      362 TCGGCATCTTATCAGATAGCCAAAGGCGAAACCA 395

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Search completed: February 8, 2004, 01:25:36
 Job time : 3142.92 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 23:41:33 ; Search time 5086.47 Seconds

(without alignments)
10809.568 Million cell updates/sec

Title: US-09-692-077D-2

Perfect score: 1344

Sequence: 1 atgagaccaccagagaccctca.....ggaccagagagcgctgtga 1344

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 30

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Geneml.*

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2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sre.*
12: gb_sy.*
13: gb_un.*
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16: em_fun.*
17: em_hum.*
18: em_in.*
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40: em_htgo_mus.*
41: em_htgo_other.*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1344	100.0	1344	6	AX350490	AX350490 Sequence
2	1344	100.0	1344	9	AF316895	AF316895 Homo sapi
3	1242	92.4	22842	9	AC092603	AC092603 Homo sapi
4	902	67.1	1353	6	AX350489	AX350489 Sequence
5	902	67.1	2072	6	AR270618	AR270618 Sequence
6	902	67.1	2072	6	HUMADRA2RA	M34041 Human alpha
7	902	67.1	3274	6	AX548756	AX548756 Sequence
8	902	67.1	9842	9	AF005900	AF005900 Homo sapi
9	605	45.0	885	9	HUMA2C2	M38742 Human alpha
10	558	41.5	828	10	S67316	S67316 alpha 2-adr
11	341	25.4	1030	9	HSAB25747	AJ325747 Homo sapi
12	230	17.1	249	10	S67320	S67320 alpha 2-adr
13	158	11.8	1194	4	SC1315936	AJ1315936 Scrocin
14	143	10.6	246	10	S6731782	S6731782 alpha 2-adr
15	137	10.2	1150	4	CSP251181	AJ251181 Cynopteri
16	127	9.4	1149	4	AF337539	AF337539 Pteropus
17	119	8.9	1185	10	GG427258	AJ427258 Gliosis
18	116	8.6	1168	4	TTA251187	AJ251187 Typha ta
19	110	8.2	1172	10	ARU427256	AJ427256 Apidontia
20	109	8.1	130	10	S6731781	S6731781 alpha 2-adr
21	107	8.0	1176	10	SVU315942	AJ315942 Scirtus v
22	101	7.5	1149	4	CUN427371	AJ427371 Cabassous
23	101	7.5	1162	4	FCA251174	AJ251174 Felis cat
24	98	7.3	1165	4	DRI251184	AJ251184 Dicerus b
25	97	7.2	1174	4	ERA2ABREC	Y12521 Erinaceus e
26	95	7.1	1156	4	MLA251107	AJ251107 Micropota
27	95	7.1	1180	4	LPA505821	AJ505821 Lama paco
28	95	7.1	1197	4	LPA315941	AJ315941 Lama paco
29	95	7.1	1356	4	AY150333	AY150333 Tupia be
30	90	6.7	1177	4	BPH251175	AJ251175 Balaenopt
31	89	6.6	1179	10	DNI427257	AJ427257 Pyromys n
32	87	6.5	1174	4	PCA427417	AJ427417 Phyleter
33	87	6.5	1176	4	LAL315940	AJ315940 Lagomorphy
34	86	6.4	1153	4	ETV17692	Y17692 Echinospe te
35	86	6.4	1168	4	PVI251176	AJ251176 Pococa vit
36	86	6.4	1179	4	CDI315943	AJ315943 Cyclopes
37	83	6.2	1171	4	DDAR28	Y15947 Dugong dugo
38	80	6.0	1185	10	EDO427270	AJ427270 Erethizon
39	77	5.7	1119	4	PMA427372	AJ427372 Pridonthe
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ALIGNMENTS

RESULT 1	AX350490	1344 bp	DNA	linear	PAT 06-FEB-2002
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DEFINITION	Sequence 2 from Patent WO0179561.				
ACCESSION	AX350490				
VERSION	AX350490.1	GI:18616092			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Liggett, S.B. and Small, K.M.				
TITLE	Alpha-2 adrenergic receptor polymorphisms				
JOURNAL	Patent: WO 0179561-A 2 25-OCT-2001;				

Pred. No. is the number of results predicted by chance to have a

AUTHORS	Waterston, R. H.
TITLE	Direct Submission
JOURNAL	Submitted (20-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	5 (bases 1 to 22842)
AUTHORS	Waterston, R. H.
TITLE	Direct Submission
JOURNAL	Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	6 (bases 1 to 22842)
AUTHORS	Waterston, R.
TITLE	Direct Submission
JOURNAL	Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT	On Oct 20, 2001 this sequence version replaced at 114016108

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPheron, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The PRC1-11 human BAC library was made from the blood of one male donor, as described by Osogoewa, K., Moon, P. Y., Zhao, B., Frengen, E., Tatom, M., Cataneese, J. J., and de Jong, P. J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

the clone sequenced to the left is RP11-401C3, 2000 bp overlap; the clone sequenced to the right is RP11-574O17, 2000 bp overlap. Actual end of this clone is at base position 48999 of RP11-574O17.

have been identified between AC013272 and AC092603.

The sequence of AC073396 has been incorporated into AC092603.
Location/Qualifiers

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Best Local Similarity 99.9%; Pred. No. 0;
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QY 841 GGCAGAGGACCAAGAGAGGTGTTTGTGGGCACTTCCAGAGATGAAGTGAAGAGAG 900
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LOCUS AX350489
DEFINITION Sequence 1 from Patent WO0179561.
ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patient: WO 0179561-A 1.25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 1181 from patent US 6500938.
ACCESSION AR270618
VERSION AR270618.1 GI:29701852
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2072)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1181 31-Dec-2002;
FEATURES
source Location/Qualifiers
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BASE COUNT 316 a 705 c 660 g 391 t
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Query Match 67.1%; Score 902; DB 6; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0;
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QY 1 ATGACACACGAGGACCCCTACTCTCCGTCAGGCGCAACAGGCGGCATATAGCGGCGGCATCAC 60
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LOCUS Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
DEFINITION M34041
ACCESSION M34041.1 GI:178197
VERSION alpha-2-adrenergic receptor; plasma membrane protein;
KEYWORDS receptor-coupled G protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2072)
Lomaney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W.,
Yang-Feng, T.L., Caron, M.G., and Lefkowitz, R.J.
Expansion of the alpha-2-adrenergic receptor family: cloning and
characterization of a human alpha-2-adrenergic receptor subtype,
the gene for which is located on chromosome 2
Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
90311349
MEDLINE 2164221
COMMENT Original source text: Human placenta DNA, clone alpha-2 C2.
Draft entry and computer-readable sequence for (1) kindly submitted
by J.W.Lomaney, 03-MAY-1990, for release after publication.

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Db 1253 GGCACAGGCGAGAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG 1312

QY 901 GA 902
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Db 1313 GA 1314

RESULT 7
AX548756 3274 bp DNA linear PAT 26-NOV-2002
LOCUS AX548756
DEFINITION Sequence 41 from Patent WO02061087.
ACCESSION AX548756
VERSION AX548756.1 GI:25813686
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Burner, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides

JOURNAL Patent: WO 02061087-A 41 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES Location/Qualifiers
Source 1..3274
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Query Match 57.1%; Score 902; DB 6; Length 3274;
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Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 781 ACCCTGAGAGATCTGTGAGACCCGCGCTTGTGCAACCAATGCTGTGCGCTTCCCAATCTCA 840
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QY 901 GA 902
DB 901 GA 902

RESULT 8

AF005900 9842 bp DNA linear PRI 08-JUL-1997
LOCUS Homo sapiens alpha2B-adrenergic receptor (alpha2C2AR) gene,
complete cds.
ACCESSION AF005900
VERSION AF005900.1 GI:2245627

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

REFERENCE 1 (bases 1 to 9842)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Cayla, C., Schak, S., Bouloumie, A., Davedjian, J.C. and Paris, H.

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9842)
Cayla, C., Schak, S., Bouloumie, A., Davedjian, J.C. and Paris, H.

AUTHORS Direct Submission
TITLE Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,
CHU Rangueil, Toulouse 31403, France

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BASE COUNT 8649..8654
ORIGIN 1870 a 2747 c 3225 g 1998 t 2 others

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Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 5518 CGCTGCTGCGCGCCCTCAGAACCTGTTCTGCTGCTGCGCGCGCCGACATCTGT 5577
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Mon Feb 9 08:28:40 2004

us-09-692-077d-2.olsigo.rge

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Db 556 TCAGGCCAGGGCCAGAGAGGGTGTGTTGGGGCATCTCCAGAGATGAGGCGAGAG 615
QY 898 GAGGA 902
Db 616 GAGGA 620

RESULT 10
S67316 828 bp mRNA linear ROD 21-APR-2003
LOCUS S67316 alpha 2-adrenergic receptor [rats, Sprague-Dawley, islets of
DEFINITION Langerhans, mRNA partial, 828 nt].
ACCESSION S67316.1 GI:456949
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 828)
AUTHORS Wang S.Y. and Pilkey, D.T. of Langerhans of a new rat alpha
TITLE Identification in islets of Langerhans of a new rat alpha
2-adrenergic receptor
DIABETES 43 (1), 127-136 (1994)
JOURNAL
MEDLINE 9408565
PUBMED 8262309
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI gi456949] from the original journal article.
This sequence comes from Fig. 1.
Location/Qualifiers
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QY 367 AAGGCAACCCCGCGCGCGCATCAAGTGCATCTCTCACTGTGGCTCATGCGCGCGTC 426
Db 82 AAGGCAACCCCGCGCGCGCATCAAGTGCATCTCTCACTGTGGCTCATGCGCGCGTC 141
QY 427 ATCTGGCGCGCGCGCTCATCAAGGGCGACAGAGGCGCGCGCGCGCGCGCGCC 486
Db 142 ATCTGGCGCGCGCGCTCATCAAGGGCGACAGAGGCGCGCGCGCGCGCGCGCC 201
QY 487 CAGTCAAGCTCAACGAGAGGCTGTGATCTTGGCTCCAGATCGATCTTTCTT 546

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Db 202 CAGTCAAGCTCAACGAGAGGCTGTGATCTTGGCTCCAGATCGATCTTTCTT 261
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Db 262 GCTCTTCTCATCATGATGATCTTGTCTACCTGGCATCTACATGATCGCAACGAGC 381
QY 607 AAGCGAGAGTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 726
Db 322 AAGCGAGAGTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 441
QY 667 CCGGACCACTGTGGGCTTTGGCTTCAAGCAAACTGCAGACCTGCTCTGTGGCTTCT 786
Db 382 CCGGACCACTGTGGGCTTTGGCTTCAAGCAAACTGCAGACCTGCTCTGTGGCTTCT 501
QY 727 GCAGAGAGTCAACGAGCACTGAAGTCACTGGGAGAGAGAGAGAGAGAGAGAGAG 846
Db 442 GCAGAGAGTCAACGAGCACTGAAGTCACTGGGAGAGAGAGAGAGAGAGAGAGAG 561
QY 787 GAGATACTGGGACCGCGGCTTGGCCACCACTGGGCTTGGCTTCCAACTCAGGCGAG 906
Db 502 GAGATACTGGGACCGCGGCTTGGCCACCACTGGGCTTGGCTTCCAACTCAGGCGAG 621
QY 847 GCGCAAGAGAGGCTTTGTGGGCACTTCAGAGATGAGAGAGAGAGAGAGAGAGAG 966
Db 562 GCGCAAGAGAGGCTTTGTGGGCACTTCAGAGATGAGAGAGAGAGAGAGAGAGAG 681
QY 907 GAGAGAGAGAGTGAACCCAGGAGTCAAGTCTCCGCGCTCAGCTTCCAGAGAGAG 1026
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RESULT 11
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LOCUS HSA325747 Homo sapiens genomic sequence surrounding Not1 site, clone
DEFINITION HSI-8185.
ACCESSION AJ325747
VERSION AJ325747.1 GI:15870141
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1030)
AUTHORS Kutsenko, A.S., Ginzburg, R.Z., Al-Amin, A.N., Wang, F., Krasna, S.M.,
Podolsky, R.M., Matsumoto, Y.G., Ganchandani, A., Kishida, V.I.,
Levitsky, V.G., Kolobanov, N.A., Protodopov, A.I., Zabarovsky, B.R.,
Kiselev, L.L., Wasserman, W., Wahlstedt, C. and Zabarovsky, B.R.
TITLE Not1 flanking sequences: a tool for gene discovery and verification
of the human genome.
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22331767
PUBMED 12136098
REMARK 2 (bases 1 to 1030)
AUTHORS Zabarovsky, B.R.
TITLE Direct Submission
JOURNAL Microbiology and Tumorigenesis Centre,
Submitted (16-MAY-2001) Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
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OY	651	TCAGCCAAATGCGCAGCCCTGGCTCTGTGGTTTCTGCGCAGAGAGTCAAGGACATCG	750		
DB	388	TCAGCCAAATGCGCAGCCCTGGCTCTGTGGTTTCTGCGCAGAGAGTCAAGGACATCG	329		
OY	751	AAGTCACCTGGGAGAGAGAGAGGGGAGACCCCTGAAGATPACTGGGACCGGGCTTG	810		
DB	328	AAGTCACCTGGGAGAGAGAGAGGGGAGACCCCTGAAGATPACTGGGACCGGGCTTG	269		
OY	811	CCACCCAGTTGGGCTGCCCTTCCCACTCAGGCCAGGGCCAGAAAGAGGTTTGTGGG	870		
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DB	208	GCATCTCCAGAGATGAAGCTGAGAGAGAGA 177			
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DEFINITION	alpha 2-adrenergic receptor [rats, Sprague-Dawley, 22 month old				
ACCESSION	S67320				
VERSION	S67320.1	GI:456953			
KEYWORDS					
SOURCE	Rattus sp.				
ORGANISM	Rattus sp.				
REFERENCE	1 (bases 1 to 249)				
AUTHORS	Wang,S.Y. and Pilkey,D.T.				
TITLE	Identification in islets of Langerhans of a new rat alpha				
JOURNAL	2-adrenergic receptor				
MEDLINE	Diabetes 43 (1), 127-136 (1994)				
PUBMED	94085695				
REMARK	8262309				
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QY	436	CCGCGCGCGCATCTACAAAGGGGAGACGAGGCGCCCAAGCCCGCGCGCGCCCAATGCGAG	495
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QY	496	CTCAACGAGAGGCGCTGGTATCATCTCGGCGCTCCAGCATCCGATCTTTCTT	545
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LOCUS	SC1315936	1194 bp	DNA linear
DEFINITION	Sorex cinereus partial adra2b gene for alpha 2B adrenergic receptor.		
ACCESSION	AJ315936		
VERSION	AJ315936.1	GI:21212915	
KEYWORDS	adra2b gene; alpha 2B adrenergic receptor.		
SOURCE	Sorex cinereus (cinereus shrew)		
ORGANISM	Sorex cinereus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.		
AUTHORS	Murphy, W.J., Eizirik, E., O'Brien, S.J., Madsen, O., Scally, M., Donad, C.J., Teeling, E., Ryder, O.A., Stanhope, M.J., de Jong, W.M. and Springer, M.S.		
TITLE	Resolution of the early placental mammal radiation using Bayesian phylogenetics		
JOURNAL	Science 294 (5550), 2348-2351 (2001)		
MEDLINE	11743200		
PUBMED	11743200		
REFERENCE	2 (bases 1 to 1194)		
AUTHORS	Madsen, O.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-AUG-2001) Madsen O., 161 Biochemistry NWI, University of Nijmegen, P.O.Box 9101, 6500 HB Nijmegen, NETHERLANDS		
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QY	181	GTGGCCACGCTCATCATCCCTTTCTGCTGCGACCAAGAGCTGCTGAGCTACTGTA	240

Search completed: February 8, 2004, 04:51:29
Job time : 5089.47 secs

Query Match	100.0%;	Score 1344;	DB 23;	Length 1344;
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 QY 601 CGGAGCAACCGGAGAGTCCAGAGGCGCAAGGGGCGGCGTGGCAGAGGATCCAAACAG 660
 Db 601 CGGAGCAACCGGAGAGTCCAGAGGCGCAAGGGGCGGCGTGGCAGAGGATCCAAACAG 660

Db	601	CCGACGAAACCGCAGAGGCTCCAGGGGCCAAGGGGGGGCGCTGGGCGAGGTGAGTCCAAACGAG	660
QY	661	CCCCGACCCGACCAATGATGGGGGCTTTTGAGCCCTCAGCCAAACTGCGCAGCCCTGGGCTCTGTG	720
Db	661	CCCCGACCCGACCAATGATGGGGGCTTTTGAGCCCTCAGCCAAACTGCGCAGCCCTGGGCTCTGTG	720
QY	721	GCTTCTGCGCAGAGAGGTCAACGGACACTTCGAGTCCACTGGGGAGAAAGAGAGGGGGAG	780
Db	721	GCTTCTGCGCAGAGAGGTCAACGGACACTTCGAGTCCACTGGGGAGAAAGAGAGGGGGAG	780
QY	781	ACCCCTGAAAGTACTGGGACCCGGGCGCTTGTGCACCCAGTTGGGCTGCGCTCCCACTCA	840
Db	781	ACCCCTGAAAGTACTGGGACCCGGGCGCTTGTGCACCCAGTTGGGCTGCGCTCCCACTCA	840
QY	841	GGCAGGAGCCGAGAAAGGAGGGTGTTTGTGGGGCATCTTCACAGAGATGAACCTGAAGAGAG	900
Db	841	GGCAGGAGCCGAGAAAGGAGGGTGTTTGTGGGGCATCTTCAGAGATGAACCTGAAGAGAG	900
QY	901	GAGAGGAGGAGGAGAGAGTGTGAACCCAGAGCAGTGGCCAGTGTCTCCGGCTCACTTGGC	960
Db	901	GAGAGGAGGAGGAGAGAGTGTGAACCCAGAGCAGTGGCCAGTGTCTCCGGCTCACTTGGC	960
QY	961	AGCCCCCGGTGAGAGAGCAACAGGCTTCCGGGTGCTGGCACCCTACGTGGCCAGAGTG	1020
Db	961	AGCCCCCGGTGAGAGAGCAACAGGCTTCCGGGTGCTGGCACCCTACGTGGCCAGAGTG	1020
QY	1021	CTCTCTGGGCGAGGGCGCTGGTGTCTTAAGTGGGCGAGTGGCCGTCCGAAGGGCCCACTG	1080
Db	1021	CTCTCTGGGCGAGGGCGCTGGTGTCTTAAGTGGGCGAGTGGCCGTCCGAAGGGCCCACTG	1080
QY	1081	ACCCGGGAGAAACGCTTCAACCTGTGTGTGGCTGTGTCAATGGCGTTTGTGTGCTGTG	1140
Db	1081	ACCCGGGAGAAACGCTTCAACCTGTGTGTGTGGCTGTGTCAATGGCGTTTGTGTGCTGTG	1140
QY	1141	TGGTTCCTCTTCTTCAAGCTAAGCCTGGGCGCCATCTGGCCGAAAGCACTGCAAGGTG	1200
Db	1141	TGGTTCCTCTTCTTCAAGCTAAGCCTGGGCGCCATCTGGCCGAAAGCACTGCAAGGTG	1200
QY	1201	CCCCATGGGCGCTTCCAGTCTCTTCTTGAGATGGGCTACTGCAACAGCTCACTGAACCTT	1260
Db	1201	CCCCATGGGCGCTTCCAGTCTCTTCTTGAGATGGGCTACTGCAACAGCTCACTGAACCTT	1260
QY	1261	GTTATCTAACCAATCTTCAACAGAGACTTCCGCGGTGGCCCTCCGGAGAGATCTGTGGCGC	1320
Db	1261	GTTATCTAACCAATCTTCAACAGAGACTTCCGCGGTGGCCCTCCGGAGAGATCTGTGGCGC	1320
QY	1321	CCGTGAGCCGAGAGCGGCGTGGTGA 1344	
Db	1321	CCGTGAGCCGAGAGCGGCGTGGTGA 1344	

RESULT 2	
ID	AAD04761
AA	AAD04761 standard; DNA; 1344 BP.
XX	
AC	AAD04761;
XX	
DT	04-JUL-2001 (first entry)
XX	
DE	Human alpha2b-adrenoceptor (alpha2b-AR) variant gene.
XX	
KW	Human; cardiant; gene therapy; alpha2b-adrenoceptor; alpha2b-AR;
KW	glutamic acid repeat; intracellular loop; chromosome 2; catecholamine
KW	norepinephrine; epinephrine; therapy; vascular contraction; variant;
KW	coronary artery; coronary heart disease; CHD; chronic angina pectoris;
XX	acute myocardial infarction; AMI; Prinzmetal's variant; ds.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	1..1344
CDS	/tag= a
FT	/product= "Human alpha2b-adrenoceptor (alpha2b-AR)"
FT	

FT	variant protein"
XX	WM0200129082-A1.
XX	26-APR-2001.
XX	20-OCT-2000; 2000MO-F100913.
XX	22-OCT-1999; 99US-0422985.
XX	(JUVVA-) JUVANTIA PHARMA LTD OY.
XX	Snapiir A, Heinoenen P, Alhopuro P, Karonen M, Koulu M, Pesonen U;
XX	Salonen M, Salonen JT, Tuominen T, Lakka TA, Nyyssönen K;
XX	Salonen R, Kaunonen J, Valkonen V;
XX	WPI; 2001-300318/31.
XX	P-PSDB; AAE00989.
XX	New DNA molecule encoding variant specific adrenoceptor protein with
XX	deletion of specific amino acids located in the third intracellular
XX	loop of the polypeptide, for treating vascular contraction of coronary
XX	arteries -
XX	Claim 3; Page 24-26; 37pp; English.
XX	The present sequence is a gene encoding human alpha2B-adrenoceptor
XX	(alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
XX	element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
XX	18 amino acids (amino acids 294-311) located in the third intracellular
XX	loop of the receptor polypeptide. The variant is obtained by deletion of
XX	three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
XX	gene is located on chromosome 2. Alpha2-AR mediate many of the
XX	physiological effects of the catecholamines, norepinephrine and
XX	epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
XX	a mammal suffering from vascular contraction of coronary arteries and a
XX	disease involving vascular contraction of coronary arteries which is
XX	clinically expressed as coronary heart disease (CHD), unstable chronic
XX	angina pectoris which is clinically expressed as Prinzmetal's variant
XX	form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
XX	gene therapy.
XX	Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
XX	Query Match 88.6%; Score 1191; DB 22; Length 1344;
XX	Best Local Similarity 99.8%; Pred. No. 0.
XX	Matches 1341; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
QY	1 ATGAGCACACGAGACCCCTACTCTCGTGCAGGCGCCCATAGCGGCGCATCAC 60
DB	1 ATGAGCACACGAGACCCCTACTCTCGTGCAGGCGCCCATAGCGGCGCATCAC 60
QY	TTCCATCTTCTTACCATCTTGGGCAACGCTGTCATCTGGCTGTGTGACAGGC 120
DB	TTCCATCTTCTTACCATCTTGGGCAACGCTGTCATCTGGCTGTGTGACAGGC 120
QY	CGCTGCTGCGCGCCCTCAGAACCTGTTCTGTGTGCTGCGCGCGCCGACATCTGT 180
DB	CGCTGCTGCGCGCCCTCAGAACCTGTTCTGTGTGCTGCGCGCGCCGACATCTGT 180
QY	GTGGCGCATGCTCATCATCTTCTTCTGCTGCGCGCAACGAGCTGCTGCTGCTGCT 240
DB	GTGGCGCATGCTCATCATCTTCTTCTGCTGCGCGCAACGAGCTGCTGCTGCTGCT 240
QY	CGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB	CGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY	GTGACACTGTGCGGCATCAGCTGAGACCGCTTACTGGGCGCTGTGAGCCGCGCTGAGTAC 360
DB	GTGACACTGTGCGGCATCAGCTGAGACCGCTTACTGGGCGCTGTGAGCCGCGCTGAGTAC 360
QY	AACCTCAAGCGCACCCCGCGCGCATCAAGTGCATCATCTTCATCTGTGTGCTCATCGCC 420

[illegible]

DT	13-DEC-2002	(first entry)
XX	Human alpha-2B-adrenoceptor variant DNA.	
DE	Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;	
XX	hypertension; hypotensive; variant; gene; ds.	
KM	Homo sapiens.	
XX	Synthetic.	
OS		
XX		
FM	Key	Location/Qualifiers
FT	CDS	1..1344
FT		/*tag= a
FT		/product= "Human alpha-2B-adrenoceptor variant
FT		protein"
XX		
PM	WO200266617-A1.	
XX		
PD	29-AUG-2002.	
XX		
PF	13-FEB-2002; 2002WO-FI00113.	
XX		
PR	20-FEB-2001; 2001FI-0000323.	
XX		
PA	(JURI-) JURILAB LTD OY.	
PI	Salonen J;	
XX		
DR	WPI; 2002-667063/71.	
XX	P-PSDB; AME26633.	
XX		
PT	Detecting a risk of hypertension and targeting treatment in a subject	
PT	by determining the pattern of alleles encoding a variant	
PT	alpha-2-adrenoceptor	
PS	Disclosure; Page 24-26; 35pp; English.	
XX		
CC	The invention relates to a method for detecting a risk of hypertension	
CC	by determining the pattern of alleles encoding a variant alpha-2B-	
CC	adrenoceptor (AR) protein. The methods and compositions of the invention	
CC	are useful for detecting risks and targeting treatment for hypertension.	
CC	The kit is also useful for selecting for clinical drug trials testing	
CC	the antihypertensive effect of compounds. The present sequence is human	
CC	alpha-2B-adrenoceptor variant DNA.	
SQ	Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;	
XX		
Query Match	88.6%; Score 1191; DB 24; Length 1344;	
Best Local Similarity	99.8%; Pred. No. 0;	
Matches 1341; Conservative	0; Mismatches 3; Indels 0; Gaps 0	
OY	1 ATGAGACCAACGAGACCCCTTACTTCGTCGACAGGCAAGCGGCATAGCGGCGCATACCC	60
Db	1 ATGAGACCAACGAGACCCCTTACTTCGTCGACAGGCAAGCGGCATAGCGGCGCATACCC	60
OY	61 TTCCCATCTTCTTTACCATCTTGGCAACGCTGTGATCATCTGGCTGTGTGAACAGC	120
Db	61 TTCCCATCTTCTTTACCATCTTGGCAACGCTGTGATCATCTGGCTGTGTGAACAGC	120
OY	121 CGCTGCTGCGCGCCCTTCAGAACCTGTTCGTGTGTGCTGGCGCGCGGCACATCTTG	180
Db	121 CGCTGCTGCGCGCCCTTCAGAACCTGTTCGTGTGTGCTGGCGCGCGGCACATCTTG	180
OY	181 GTGGCGACGCTCATATCCCTTTCGCTGGGCAACGAGCTGTGGCTACCTGTGATCTC	240
Db	181 GTGGCGACGCTCATATCCCTTTCGCTGGGCAACGAGCTGTGGCTACCTGTGATCTC	240
OY	241 CGGCGCAGTGTGTGAGAGGTGTACCTGTGGCGCTGTGACGTCTTTGTGACCTGTGATC	300
Db	241 CGGCGCAGTGTGTGAGAGGTGTACCTGTGGCGCTGTGACGTCTTTGTGACCTGTGATC	300
OY	301 GTGACACTGTGTGCGCATACAGCTGTGACCGGCTACTGTGGCCGTGTGACCGCGCGCTGTGAGATAC	360

Db	301	GTGACCTGTGCGGCATTAAGCCTGGAACGGCTACTGAGCCGTGAGCCGCGCGCTTGAGATAC	360
Qy	361	AACTTCAAAGGGAACCCGCGCGCGCATCAAGTGCATCATCTTCACTGTGTGCTCATCGCC	420
Db	361	AACTTCAAAGGGAACCCGCGCGCGCATCAAGTGCATCATCTTCACTGTGTGCTCATCGCC	420
Qy	421	GGCGTCATCTGCTGCGCGCCCTCATCTTACAAGAGGCGACAGAGGCGCCCAAGCGCGCGG	480
Db	421	GGCGTCATCTGCTGCGCGCCCTCATCTTACAAGAGGCGACAGAGGCGCCCAAGCGCGCGG	480
Qy	481	CGCCCCCAGTGCDAAGTCAACCAAGAGGCTGTGATCATCTTGCTCCAGCATCGATCT	540
Db	481	CGCCCCCAGTGCDAAGTCAACCAAGAGGCTGTGATCATCTTGCTCCAGCATCGATCT	540
Qy	541	TTCTTTGGTCTTGTGCTCATCATGATTCCTTGATCACTGGCGATCTTACCTGATTCGCAAA	600
Db	541	TTCTTTGGTCTTGTGCTCATCATGATTCCTTGATCACTGGCGATCTTACCTGATTCGCAAA	600
Qy	601	CGACGCAACCGCAGAGGTCCGAGGCGCAAGGAGGAGGCTGTGGCAGAGTGAATCAACAG	660
Db	601	CGACGCAACCGCAGAGGTCCGAGGCGCAAGGAGGAGGCTGTGGCAGAGTGAATCAACAG	660
Qy	661	CCCCGACCCGACCATGTGTGGGGCTTTGGCCTTCAGTCAAACTGACAGCCCTTGCCCTGTG	720
Db	661	CCCCGACCCGACCATGTGTGGGGCTTTGGCCTTCAGTCAAACTGACAGCCCTTGCCCTGTG	720
Qy	721	GCTTCTGCAAGAGTTCACGACACTCGAAGTCACTGGAGSAAAGAGAGAGGAGGAG	780
Db	721	GCTTCTGCAAGAGTTCACGACACTCGAAGTCACTGGAGSAAAGAGAGAGGAGGAG	780
Qy	781	ACCCCTGAAGTACTGGGACCCCGGAGCTTTGGCAACCAGTTGGAGCTGCCCTTCCAACTCA	840
Db	781	ACCCCTGAAGTACTGGGACCCCGGAGCTTTGGCAACCAGTTGGAGCTGCCCTTCCAACTCA	840
Qy	841	GGCCAGGGCCCGAAGAGAGGTGTTGTGTGGGCATCTCAGAGSAGTGAAGCTGAAGAGAG	900
Db	841	GGCCAGGGCCCGAAGAGAGGTGTTGTGTGGGCATCTCAGAGSAGTGAAGCTGAAGAGAG	900
Qy	901	GAGGAGGAGGAGGAAGAGTGAACCCAGGCAAGTGCAGTGTCTCGAGCTCAGCTTGC	960
Db	901	GAGGAGGAGGAGGAAGAGTGAACCCAGGCAAGTGCAGTGTCTCGAGCTCAGCTTGC	960
Qy	961	AGCCCCCGCTGCGAGGCAACAGAGGCTCCGAGGCTGGGCAACCTTACGTGGCCAGAGG	1020
Db	961	AGCCCCCGCTGCGAGGCAACAGAGGCTCCGAGGCTGGGCAACCTTACGTGGCCAGAGG	1020
Qy	1021	CTCTGTGGCAGAGGCGTGGGTGCTATATAGTGGGCAAGTGTGGCGCTCGAAGGCGCAGCTG	1080
Db	1021	CTCTGTGGCAGAGGCGTGGGTGCTATATAGTGGGCAAGTGTGGCGCTCGAAGGCGCAGCTG	1080
Qy	1081	ACCGGGAGGAAGGCTTCAACCTTGATGTGGCTGTGATCAATTTGGGCTTTTGTGTGCTG	1140
Db	1081	ACCGGGAGGAAGGCTTCAACCTTGATGTGGCTGTGATCAATTTGGGCTTTTGTGTGCTG	1140
Qy	1141	TGTTTCCCTTCTTCAAGCTACAGCCTTGAGGTGAGCTTCAATTTGGGCTTTTGTGTGCTG	1200
Db	1141	TGTTTCCCTTCTTCAAGCTACAGCCTTGAGGTGAGCTTCAATTTGGGCTTTTGTGTGCTG	1200
Qy	1201	CCCCATAGGCGCTTCCAGTCTTCTTCTTGATTCGGCTATCTGCAACAGCTCACTGAACCTT	1260
Db	1201	CCCCATAGGCGCTTCCAGTCTTCTTCTTGATTCGGCTATCTGCAACAGCTCACTGAACCTT	1260
Qy	1261	GTTATCTACACCATCTTCAACAGAGACTTCGCGGTGCTTTCGGAGAGATCCTGTGCGCG	1320
Db	1261	GTTATCTACACCATCTTCAACAGAGACTTCGCGGTGCTTTCGGAGAGATCCTGTGCGCG	1320
Qy	1321	CCGTGGAACCAAGACGCGCTGTGTA 1344	
Db	1321	CCGTGGAACCAAGACGCGCTGTGTA 1344	

RESULT 4

AA04762
ID AAD04762 standard; DNA; 1353 BP.
XX
AC AAD04762;
XX
DT 04-JUL-2001 (first entry)
DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX
KW Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
norepinephrine; epinephrine; therapy; vascular contraction;
coronary artery; coronary heart disease; CHD; chronic angina pectoris;
acute myocardial infarction; AMI; Prinzmetal's variant; de.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1353
FT /tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
protein"
XX
XX MO200129082-A1.
XX
XX PD 26-APR-2001.
XX
XX PF 20-OCT-2000; 2000MO-F100913.
XX
XX PR 22-OCT-1999; 99US-0422985.
XX
XX (JUVVA-) JUVVANTIA PHARMA LTD OY.
XX
XX PI Snapiir A., Heikonen P., Alhopuro P., Karvonen M., Koulou M., Pesonen U;
PI Scheinin M., Salonen JT., Tuomainen T., Lakka TA., Nyyssoenen K;
PI Salonen R., Kahkonen J., Valkonen V;
XX
XX WPI; 2001-300318/31.
XX
XX P-PSDB; AAE00990.
XX
XX PT New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular
PT loop of the polypeptide, for treating vascular contraction of coronary
PT arteries -
XX
XX PS Disclosure; Page 27-29; 37pp; English.
XX
XX CC The present sequence is a gene encoding human alpha2B-adrenoceptor
CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
CC acids (amino acids 294-311) located in the third intracellular loop of
CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
CC Alpha2-AR mediate many of the physiological effects of the
CC catecholamines, norepinephrine and epinephrine. An antagonist of
CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
CC vascular contraction of coronary arteries and a disease involving
CC vascular contraction of coronary arteries which is clinically expressed
CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
CC clinically expressed as Prinzmetal's variant form or acute myocardial
CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
XX
XX SO Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
Query Match 67.1%; Score 902; DB 22; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 61 TTCCTCATCTCTTTACATCTTCGCGAAGCTCTGCTCATCTCGCTGTGTGACGAGC 120
QY CGCTCGTGGGCGCCCTCGAAGACTGTTCGTGTGCTGCGCGCGCGCGCATCTCG 180
DB 121 CGCTCGTGGGCGCCCTCGAAGACTGTTCGTGTGCTGCGCGCGCGCGCATCTCG 180
QY 181 GTGGCCACGCTCATCATCTCTTTCTGCTGGCCCAAGAGCTGTGGGCTACTGTGACTTC 240
DB 181 GTGGCCACGCTCATCATCTCTTTCTGCTGGCCCAAGAGCTGTGGGCTACTGTGACTTC 240
QY 241 CGGCGCACTGTGCGAAGGTGTAAGTGTGCTGAGCTGTCTTCTGCACTGTCTCATC 300
DB 241 CGGCGCACTGTGCGAAGGTGTAAGTGTGCTGAGCTGTCTTCTGCACTGTCTCATC 300
QY 301 GTGCACTGTGCGAAGGTGTAAGTGTGCTGAGCTGTCTTCTGCACTGTCTCATC 360
DB 301 GTGCACTGTGCGAAGGTGTAAGTGTGCTGAGCTGTCTTCTGCACTGTCTCATC 360
QY 361 AACTCGAAGCGAAGCGCGCGCGCGCATCAAGTGCATCTCTGCTGTGCTCATCTGCC 420
DB 361 AACTCGAAGCGAAGCGCGCGCGCGCATCAAGTGCATCTCTGCTGTGCTCATCTGCC 420
QY 421 GCCGTATCTCGCTGCGCGCGCGCGCATCTCAAGAGGCGACCGCGCGCGCGCGCG 480
DB 421 GCCGTATCTCGCTGCGCGCGCGCGCATCTCAAGAGGCGACCGCGCGCGCGCGCG 480
QY 481 CGGCGCGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 540
DB 481 CGGCGCGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 540
QY 541 TTCTTGTCTCTTGTCTCTCATCATCATCTTGTCTCATCTGCGCATCTGCGCAAA 600
DB 541 TTCTTGTCTCTTGTCTCTCATCATCATCTTGTCTCATCTGCGCATCTGCGCAAA 600
QY 601 CGCAGCAACCGCAGAGTTCAGAGGCGCAAGAGGCGCGCTGTGAGTGAAGTCAAGCAG 660
DB 601 CGCAGCAACCGCAGAGTTCAGAGGCGCAAGAGGCGCGCTGTGAGTGAAGTCAAGCAG 660
QY 661 CCCGACCCGACCATGTGTGGGCTTTGGCTCAGCCAACTGCGAGCCTGTGCTGTG 720
DB 661 CCCGACCCGACCATGTGTGGGCTTTGGCTCAGCCAACTGCGAGCCTGTGCTGTG 720
QY 721 GCTTTCGCGAAGAGTTCAGAGGCGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 780
DB 721 GCTTTCGCGAAGAGTTCAGAGGCGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 780
QY 781 ACCCTGAAGATTAAGTGAAGTTCGAGCGCTTGCACCAAGTGTGGCTGCTTCCCACTCA 840
DB 781 ACCCTGAAGATTAAGTGAAGTTCGAGCGCTTGCACCAAGTGTGGCTGCTTCCCACTCA 840
QY 841 GGCAGAGGCGCAAGAGAGTGTGTGTGGGCTATCTCGAGAGTGAAGTGAAGAGAG 900
DB 841 GGCAGAGGCGCAAGAGAGTGTGTGTGGGCTATCTCGAGAGTGAAGTGAAGAGAG 900
QY 901 GA 902
DB 901 GA 902
RESULT 5
ID AAI99905 standard; DNA; 1353 BP.
XX
XX AC AAI99905;
XX
XX DT 18-FEB-2002 (first entry)
XX
XX DE Human alpha-2BAR third intracellular loop encoding DNA.
XX
XX KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR;

XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT CDS 1..1353
 FT /tag a
 FT /product= "Human alpha-2B-adrenoceptor protein"
 XX PN WO200266617-A1.
 XX PD 29-AUG-2002.
 XX PF 13-FEB-2002; 2002WO-FI00113.
 XX PR 20-FEB-2001; 2001FI-0000323.
 XX PA (JURI-) JURILAB LTD OY.
 XX PI Salonen J;
 XX DR WPI; 2002-667063/71.
 XX P-PSDB; AAE26634.
 XX PT Detecting a risk of hypertension and targeting treatment in a subject
 PT by determining the pattern of alleles encoding a variant
 PT alpha-2-adrenoceptor -
 XX PS Disclosure; Page 27-29; 35pp; English.
 XX CC The invention relates to a method for detecting a risk of hypertension
 CC by determining the pattern of alleles encoding a variant alpha-2B-
 CC adrenoceptor (AR) protein. The methods and compositions of the invention
 CC are useful for detecting risks and targeting treatment for hypertension.
 CC The kit is also useful for selecting for clinical drug trials testing
 CC the antihypertensive effect of compounds. The present sequence is human
 CC alpha-2B-adrenoceptor gene.
 SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;

Query Match 67.1%; Score 902; DB 24; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCAACAGAGACCCCTACTCCGTCAGGCGACAGCGGCATAGCGGCGCATCACC 60
 DB 1 ATGAGCAACAGAGACCCCTACTCCGTCAGGCGACAGCGGCATAGCGGCGCATCACC 60
 QY 61 TTCCTCATTTCTTTACCATCTTTCGCAACGCTTGTCATCTGCTGTGTTGACACAGC 120
 DB 61 TTCCTCATTTCTTTACCATCTTTCGCAACGCTTGTCATCTGCTGTGTTGACACAGC 120
 QY 121 CGCTGCTGCGCGCCCTCTCAAGAACTGTTCTGTGTCTGTCGTCGCGCGGACATCTTG 180
 DB 121 CGCTGCTGCGCGCCCTCTCAAGAACTGTTCTGTGTCTGTCGTCGCGCGGACATCTTG 180
 QY 181 GTGGCAGCGTCATATCCCTTTCTGTCGCGCAACGACTCTGGGCTACTGTAATTC 240
 DB 181 GTGGCAGCGTCATATCCCTTTCTGTCGCGCAACGACTCTGGGCTACTGTAATTC 240
 QY 241 CGGCGCAGTGTGCGAGGTGTACCTGCGCTGACAGTCTCTTCTGCACTCGTCATC 300
 DB 241 CGGCGCAGTGTGCGAGGTGTACCTGCGCTGACAGTCTCTTCTGCACTCGTCATC 300
 QY 301 GTGCACTGTGTGCGCATCAGCTTGACCGCTACTGCGGCGGTGAGCGGCTGAGTAC 360
 DB 301 GTGCACTGTGTGCGCATCAGCTTGACCGCTACTGCGGCGGTGAGCGGCTGAGTAC 360
 QY 361 AACTCAGCGGACCCCGCGCGCGCATCAAGTGCATCTTCACTGTGTGCTCATCGCC 420
 DB 361 AACTCAGCGGACCCCGCGCGCGCATCAAGTGCATCTTCACTGTGTGCTCATCGCC 420
 QY 421 GCCGTATCTCGCTCGCGCCCTCTCATCTCAAGGGGCAACGAGGCCCGCGCGCGG 480
 DB 421 GCCGTATCTCGCTCGCGCCCTCTCATCTCAAGGGGCAACGAGGCCCGCGCGCGG 480

DB 421 GCCGTATCTCGCTCGCGCCCTCTCATCTCAAGGGGCAACGAGGCCCGCGCGG 480
 QY 481 CGCCCCAGTGAAGCTCAACAGAGAGCGCTGGTATCTCGGCGCTCAAGCATCGATCT 540
 DB 481 CGCCCCAGTGAAGCTCAACAGAGAGCGCTGGTATCTCGGCGCTCAAGCATCGATCT 540
 QY 541 TTCTTGTCTCTTGTCTCATCATGATCTTGTCTCACTGCGCATCTACCTGATCGCAAA 600
 DB 541 TTCTTGTCTCTTGTCTCATCATGATCTTGTCTCACTGCGCATCTACCTGATCGCAAA 600
 QY 601 CGAGCAACCGCAAGGTCTCCAGGCGCAAGGCGGCGCTGGCAGGCTGATCCAAACAG 660
 DB 601 CGAGCAACCGCAAGGTCTCCAGGCGCAAGGCGGCGCTGGCAGGCTGATCCAAACAG 660
 QY 661 CCCGACCGGACCATGATGAGGCTTGTGCTCAGGCCAACTGCGAGCCCTGCGCTGTG 720
 DB 661 CCCGACCGGACCATGATGAGGCTTGTGCTCAGGCCAACTGCGAGCCCTGCGCTGTG 720
 QY 721 GCTTTCGACAGAGGTCAACGCACTCGAAGTCCACTGGGAGAGAGAGAGGAGGAG 780
 DB 721 GCTTTCGACAGAGGTCAACGCACTCGAAGTCCACTGGGAGAGAGAGAGAGGAGGAG 780
 QY 781 ACCCTGAAGATATCTGAGACCCGCGCTTGCACCAAGTTGAGGCTGCTTCCAACTCA 840
 DB 781 ACCCTGAAGATATCTGAGACCCGCGCTTGCACCAAGTTGAGGCTGCTTCCAACTCA 840
 QY 841 GGCAGGCGCAGAGAGAGGTTTGTGCGGATCTCCAGAGATCAACTGAAGAGAG 900
 DB 841 GGCAGGCGCAGAGAGAGGTTTGTGCGGATCTCCAGAGATCAACTGAAGAGAG 900
 QY 901 GA 902
 DB 901 GA 902

RESULT 7
 ID ACAS6583
 ACAS6583 strand; cDNA; 2072 BP.
 ACAS6583;
 06-JUN-2003 (first entry)
 Human signalling pathway polynucleotide probe SEQ ID NO 1181.
 Human; probe; ss; array element; Parkinson's disease;
 signalling pathway population; cancer; adenocarcinoma; leukaemia;
 immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 Homo sapiens.
 US6500938-B1.
 31-DEC-2002.
 30-JAN-1998; 98US-0016434.
 30-JAN-1998; 98US-0016434.
 (INCY-) INCYTE GENOMICS INC.
 Au-Young J; Seilhamer J;
 WPI; 2003-352189/33.
 Combination of polynucleotide probes, useful as array elements in a
 microarray for monitoring the expression of a number of target
 polynucleotides -
 Claim 1; SEQ ID NO 1181; 65pp; English.
 The invention relates to a combination which, comprises a number of
 polynucleotide probes comprising a sequence selected from one of the 1490

CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.

XX Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 other;

Query Match 67.1%; Score 902; DB 25; Length 2072;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGAGACCAAGAGACCCCTACTCCGTGAGAGCCACAGGCGCCATAGGCGGCGCATACACC 60
DB 413 ATGAGACCAAGAGACCCCTACTCCGTGAGAGCCACAGGCGCCATAGGCGGCGCATACACC 472
QY 61 TTCTCTATTTCTTTTACATCTTGGAGAGCTGTGATCTGCTGTGTTGACGAGC 120
DB 473 TTCTCTATTTCTTTTACATCTTGGAGAGCTGTGATCTGCTGTGTTGACGAGC 532
QY 121 CGCTCGTGGCGCGCCCTCAGAACTTCTCTGTGTCGTGCGCGCGCGCGCATCTCTG 180
DB 533 CGCTCGTGGCGCGCCCTCAGAACTTCTCTGTGTCGTGCGCGCGCGCGCATCTCTG 592
QY 181 GTGGCAACGCTCATCATCTCTTCTCGCTGGCCACAGAGCTGCTGGGCTACTGTACTTC 240
DB 593 GTGGCAACGCTCATCATCTCTTCTCGCTGGCCACAGAGCTGCTGGGCTACTGTACTTC 652
QY 241 CGGCGACCTGTGTGCGAGGTGTAACCTGCGCTGAGAGCTGCTGTGCGCTGCTGATC 300
DB 653 CGGCGACCTGTGTGCGAGGTGTAACCTGCGCTGAGAGCTGCTGTGCGCTGCTGATC 712
QY 301 GTGCAACCTGTGCGAGGTGTAACCTGCGCTGAGAGCTGCTGTGCGCTGCTGATC 360
DB 713 GTGCAACCTGTGCGAGGTGTAACCTGCGCTGAGAGCTGCTGTGCGCTGCTGATC 772
QY 361 AACTCCAAGCGACCCCGCGCGCATCAAGTGCATCATCTGCTGTGTGCTCATGCC 420
DB 773 AACTCCAAGCGACCCCGCGCGCATCAAGTGCATCATCTGCTGTGTGCTCATGCC 832
QY 421 GCGGTATCTGTGCGCGCCCTTATCTAAGAGCGCAAGAGGCGCCCAAGCGCGGAG 480
DB 833 GCGGTATCTGTGCGCGCCCTTATCTAAGAGCGCAAGAGGCGCCCAAGCGCGGAG 892
QY 481 CGCCCGGAGTGCAGTCAACAGAGAGCGCTGTATACCTGTGCGCTGAGAGTCT 540
DB 893 CGCCCGGAGTGCAGTCAACAGAGAGCGCTGTATACCTGTGCGCTGAGAGTCT 952
QY 541 TTCTTTGCTCTTCTGCTCATCATGATCTTGTCTACTGCGCATCTAATCTGATGCCAA 600
DB 953 TTCTTTGCTCTTCTGCTCATCATGATCTTGTCTACTGCGCATCTAATCTGATGCCAA 1012
QY 601 CGGAGCAACCGGAGAGTCCAGAGGCGCAAGAGGCGGCTGTGGGAGGGTGAATCCAAAG 660
DB 1013 CGGAGCAACCGGAGAGTCCAGAGGCGCAAGAGGCGGCTGTGGGAGGGTGAATCCAAAG 1072
QY 661 CCGGAGCGGAGTGTGTGCTTGTGCTGAGCAAACTGCGAGCGCTGCTGTG 720
DB 1072 CCGGAGCGGAGTGTGTGCTTGTGCTGAGCAAACTGCGAGCGCTGCTGTG 1132
```

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DB 1073 CCGGAGCGGAGTGTGTGCTTGTGCTGAGCAAACTGCGAGCGCTGCTGTG 1132
QY 721 GCTTGTGCGAGAGGTCAACGAGACTCGAAGTCCATCTGGAGAGAGAGAGGAG 780
DB 1133 GCTTGTGCGAGAGGTCAACGAGACTCGAAGTCCATCTGGAGAGAGAGAGGAG 1192
QY 781 ACCCTGGAAGTACTGGAGACCGGCGCTTGGCCACCAAGTGGGCTGCCCTTCCAACTCA 840
DB 1193 ACCCTGGAAGTACTGGAGACCGGCGCTTGGCCACCAAGTGGGCTGCCCTTCCAACTCA 1252
QY 841 GCGCAGGCGCAGAGAGAGGTCTTGTGGGAGATCTCCAGAGAGTGAAGTGAAGAGAG 900
DB 1253 GCGCAGGCGCAGAGAGAGGTCTTGTGGGAGATCTCCAGAGAGTGAAGTGAAGAGAG 1312
QY 901 GA 902
DB 1313 GA 1314

RESULT 8
ABZ42624
ID ABZ42624 strand; DNA; 3274 BP.
XX
XX ABZ42624;
AC
XX
XX 04-MAR-2003 (first entry)
DT
XX
XX
DE Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer; gene; de.
XX
XX Homo sapiens.
OS
XX
XX MO200261087-A2.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 19-DEC-2001; 2001WO-US50107.
PF
XX
XX 19-DEC-2000; 2000US-257144P.
PR
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
PA
XX
XX Burner GC, Roush CL, Brown JP;
PI
XX
XX WPI; 2003-046718/04.
DR
XX
XX P-FSDB; ABP81780.
DR
XX
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
PS Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising:
XX (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular
XX G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity
XX or avidity for a particular GPCR. (I) can be used as GPCR modulators and
XX in gene therapy. The antigenic peptides for GPCRs are useful in detecting
XX an antibody against a particular GPCR, and in the production of specific
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antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immun-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunosays and immunodiagnosis. AB242523 to AB242869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.

Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 other;

Query Match 67.1%; Score 902; DB 25; Length 3274;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGAGACACGAGACCCCTACTCCGTGACAGCAGCGGCATAGCGGCGCATACACC 60
DB 1 ATGAGACACGAGACCCCTACTCCGTGACAGCAGCGGCATAGCGGCGCATACACC 60
QY 61 TTCCTATTCTCTTTACCATCTTCCGCAACGCTTGGTCATCTGCTGTGTGACCAAGC 120
DB 61 TTCCTATTCTCTTTACCATCTTCCGCAACGCTTGGTCATCTGCTGTGTGACCAAGC 120
QY 121 CGCTGCTGCGGCGCCCTGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 CGCTGCTGCGGCGCCCTGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 GTGGCCACGCTCATCATCCCTTCTGCTGCGCAACGAGTGTGAGGCTACTGCTACTTC 240
DB 181 GTGGCCACGCTCATCATCCCTTCTGCTGCGCAACGAGTGTGAGGCTACTGCTACTTC 240
QY 241 CGGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 CGGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 GTGGCACTGTGCGCCCATCAAGCTGAGCCGCTACTGCGGCGGTGAGCGGCGGTGAGTAC 360
DB 301 GTGGCACTGTGCGCCCATCAAGCTGAGCCGCTACTGCGGCGGTGAGCGGCGGTGAGTAC 360
QY 361 AACTCCAGGCGACCCCGCGCGCATCAAGTGCATCATCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 AACTCCAGGCGACCCCGCGCGCATCAAGTGCATCATCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 GCGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GCGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CGGCGCGAGTGCAGCTCAACGAGGCGGTGTAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 CGGCGCGAGTGCAGCTCAACGAGGCGGTGTAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 TTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 TTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 CGGAGCAACGAGAGTCCCAAGGCGCAAGGCGGCGCTGCGGAGGAGTGCAGCAAGAG 660
DB 601 CGGAGCAACGAGAGTCCCAAGGCGCAAGGCGGCGCTGCGGAGGAGTGCAGCAAGAG 660
QY 661 CGGCGAGCGGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 CGGCGAGCGGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 GCTTCTGCGAGAGGTCAACGAGCACTGGAAGTCCACTGCGGAGGAGAGGAGGAG 780

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DB 721 GCTTCTGCGAGAGGTCAACGAGCACTGGAAGTCCACTGCGGAGGAGAGGAGGAG 780
QY 781 ACCCTGGAAGATCTGAGAACCCGGGCTTGGCCACCAAGTTGGCTGCTTCCCACTCA 840
DB 781 ACCCTGGAAGATCTGAGAACCCGGGCTTGGCCACCAAGTTGGCTGCTTCCCACTCA 840
QY 841 GCGCAGGCGCAGAGAGGAGGAGTGTGTTGGGCGCATCTCCAGAGATGAGCTGAAGAGAG 900
DB 841 GCGCAGGCGCAGAGAGGAGGAGTGTGTTGGGCGCATCTCCAGAGATGAGCTGAAGAGAG 900
QY 901 GA 902
DB 901 GA 902

```

RESULT 9

AA014151

ID AA014151 standard; DNA; 2064 BP.

XX AA014151;

AC 06-JAN-1992 (first entry)

DE Human alpha 2 beta adrenergic receptor gene.

KW Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 288..1752

FT /*tag= a

PN US053337-A.

PD 01-OCT-1991.

PF 30-OCT-1989; 89US-0428856.

PR 30-OCT-1989; 89US-0428856.

PA (NEUR-) NEUROGENETIC CORP.

PI Weinshank RL, Hartig PR;

DR WPI; 1991-310087/42.

PT P-PSDB; AAR14149.

PT Isolated DNA encoding human adrenergic receptor - for detecting

PT nucleic acids encoding alpha, 2-beta adrenergic receptor, for

PT screening drugs.

PS Claim 1; Fig 2; 15pp; English.

CC Clone NGC-alpha2beta was isolated from a human spleen genomic

CC library by screening with a fragment of the human 5-HT1A receptor

CC gene. The gene can be used to express recombinant receptor protein

CC which can be used to produce antibodies for inhibition of receptor

CC function.

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Query Match 38.8%; Score 522; DB 12; Length 2064;

Best Local Similarity 100.0%; Pred. No. 6; 3e-230;

Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 381 CGGATCAAGTGTATATCTCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 440
DB 779 CGGATCAAGTGTATATCTCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 838
QY 441 CCTCATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 500

```



```

Db      839 CCTCATCTCAAGAGGCGACGAGGCCCCAGCGCGGCGCCCCAGTGAAGTCAA 898
Qy      501 CCGAGAGGCGCTGGTATCATCTGCGCTCCAGATCGATCTTTCTTCTCTCTGCTCAT 560
Db      899 CCGAGAGGCGCTGGTATCATCTGCGCTCCAGATCGATCTTTCTTCTCTCTGCTCAT 958
Qy      561 CATGATCTCTTGTCTTACCTGCGCATCTTACCTGATCGCAAGCAGACCGAGAGTCC 620
Db      959 CATGATCTCTTGTCTTACCTGCGCATCTTACCTGATCGCAAGCAGACCGAGAGTCC 1018
Qy      621 CAGGCGCAAGGAGGAGGCGCTGAGGAGGATCGCAAGCAGCAGCAGCAGCAGTGG 680
Db      1019 CAGGCGCAAGGAGGAGGCGCTGAGGAGGATCGCAAGCAGCAGCAGCAGCAGTGG 1078
Qy      681 GGCCTTGGCGCTCAGCCAACTGCGAGCGCTGCTGCGCTGCTGCGCAAGAGGTCAA 740
Db      1079 GGCCTTGGCGCTCAGCCAACTGCGAGCGCTGCTGCGCTGCTGCGCAAGAGGTCAA 1138
Qy      741 CGGACACTCGAAGTCCAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 800
Db      1139 CGGACACTCGAAGTCCAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198
Qy      801 CCGGCGCTTGGCGCAAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
Db      1199 CCGGCGCTTGGCGCAAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1258
Qy      861 TGTGTGTGGGCGATCTCCAGAGATGAAGCTGAAGAGAGAGA 902
Db      1259 TGTGTGTGGGCGATCTCCAGAGATGAAGCTGAAGAGAGAGA 1300

```

RESULT 10

AAT59499 standard; DNA; 2064 BP.

AAT59499;

25-MAR-2003 (updated)
06-MAY-1997 (first entry)

Human alpha-2b adrenergic receptor genomic DNA clone.

Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
epinephrine; signal transduction; neurotransmitter; ligand; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 288..1751
/*tag= a

US5595880-A.

21-JAN-1997.

22-OCT-1992; 92US-0965040.

30-OCT-1989; 89US-0428856.

30-MAY-1991; 91US-0707604.

22-OCT-1992; 92US-0965040.

(SYNA-) SYNAPTIC PHARM CORP.

Hartig PR, Weinehank RL;

MP1. 1997-107576/10.

P-PSDB; AAM11804.

Assay for alpha-2b adrenergic receptor ligands - using membranes of
cells expressing recombinant receptor

Disclosure; Fig 2A-B; 16pp; English.

CC A genomic DNA clone (AAT59499) codes for human alpha-2b adrenergic
CC receptor (AAM11804), a member of the rhodopsin-like signal transducer
CC family. It was isolated from a human spleen genomic library in the
CC lambda vector Charon 28 by screening with a 1.6 kb fragment of the
CC human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2b
CC comprising DNA encoding the alpha-2b adrenoceptor is deposited as
CC ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2b
CC adrenoceptor in bacterial, yeast or mammalian cells; transfected
CC Ltk- cells, designated L-NGC-alpha-2b, are deposited as ATCC CRL
CC 10275. Membranes of such cells can used in novel methods to
CC identify drugs which specifically interact with, and bind to, the
CC alpha-2b adrenergic receptor.
CC (updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;

Query Match 38.8%; Score 522; DB 18; Length 2064;

Best Local Similarity 100.0%; Pred. No. 6.3e-230; Indels 0; Gaps 0;

Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      381 CCGGATCAAGTGCATCATCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440
Db      779 CCGGATCAAGTGCATCATCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 838
Qy      441 CCTCATCTCAAGAGGCGACAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 500
Db      839 CCTCATCTCAAGAGGCGACAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 898
Qy      501 CCGAGAGGCGCTGATCATCTGCGCTCAGAGTGGATCTTTCTTCTCTCTGCTCAT 560
Db      899 CCGAGAGGCGCTGATCATCTGCGCTCAGAGTGGATCTTTCTTCTCTCTGCTCAT 958
Qy      561 CATGATCTCTTGTCTTACCTGCGCATCTTACCTGATCGCAAGCAGACCGAGAGTCC 620
Db      959 CATGATCTCTTGTCTTACCTGCGCATCTTACCTGATCGCAAGCAGACCGAGAGTCC 1018
Qy      621 CAGGCGCAAGGAGGAGGCGCTGAGGAGGATCGCAAGCAGCAGCAGCAGCAGTGG 680
Db      1019 CAGGCGCAAGGAGGAGGCGCTGAGGAGGATCGCAAGCAGCAGCAGCAGCAGTGG 1078
Qy      681 GGCCTTGGCGCTCAGCCAACTGCGAGCGCTGCTGCGCTGCTGCGCAAGAGGTCAA 740
Db      1079 GGCCTTGGCGCTCAGCCAACTGCGAGCGCTGCTGCGCTGCTGCGCAAGAGGTCAA 1138
Qy      741 CGGACACTCGAAGTCCAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 800
Db      1139 CGGACACTCGAAGTCCAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198
Qy      801 CCGGCGCTTGGCGCAAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
Db      1199 CCGGCGCTTGGCGCAAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1258
Qy      861 TGTGTGTGGGCGATCTCCAGAGATGAAGCTGAAGAGAGAGA 902
Db      1259 TGTGTGTGGGCGATCTCCAGAGATGAAGCTGAAGAGAGAGA 1300

```

RESULT 11

ABN32100 standard; DNA; 65 BP.

ABN32100;

15-JUL-2002 (first entry)

Rat spliced transcript detection oligonucleotide SEQ ID NO:4848.

Human; mouse; rat; splice transcript; detection; RNA transcript;

splice variant; transcriptome; oligonucleotide library; ss.

Rattus norvegicus.

WO200210449-A2.


```
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-IB01903.
PF
XX 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
DR WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX Example 1; SEQ ID 4848; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 65 BP; 13 A; 22 C; 21 G; 9 T; 0 other;
SQ
XX
XX Query Match 4.8%; Score 65; DB 24; Length 65;
XX Best Local Similarity 100.0%; Pred. No. 1e-19;
XX Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 642 GCAGGTGAGTCCAGAGCCCGACCATGTGCGGCTTTGGCTTCAGCAAACT 701
DB 1 GCAGGTGAGTCCAGAGCCCGACCATGTGCGGCTTTGGCTTCAGCAAACT 60
QY 702 GCCAG 706
DB 61 GCCAG 65
XX
XX RESULT 12
XX ABN46479
XX ID ABN46479 standard; DNA; 60 BP.
XX AC
XX ABN46479;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:19227.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
```

```
XX Homo sapiens.
OS
XX
XX NO200210449-A2.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-IB01903.
PF
XX 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
DR WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX Example 1; SEQ ID 19227; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 60 BP; 13 A; 20 C; 16 G; 11 T; 0 other;
SQ
XX
XX Query Match 4.5%; Score 60; DB 24; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-17;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 698 AACTGCCAGCGCTGCGCTTGTGCTTGCAGAGAGTCAACGACACTCGAAGTCCA 757
DB 1 AACTGCCAGCGCTGCGCTTGTGCTTGCAGAGAGTCAACGACACTCGAAGTCCA 60
XX
XX RESULT 13
XX AA19917
XX ID AA19917 standard; DNA; 1350 BP.
XX AC
XX AA19917;
XX
XX 18-FEB-2002 (first entry)
XX
XX Human alpha-2AAR encoding DNA.
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX polymorphic site; allelic variant; cardiovascular disease;
XX
```

KM central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KM phosphorylation; inositol phosphate; alpha-2AR;
 KM GenBank Accession AF281308; chromosome 10; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1353
 FT /tag= a
 FT /product= "alpha-2AAR"
 XX
 PN WO200179561-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US12575.
 XX
 PR 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 XX
 PS WPI: 2001-611728/70.
 DR P-PSDB; AAM52122.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Example 7; Page 151; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (999GCG99GCG) or (B) (999GCGCTGAG) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2AAR gene
 CC (GenBank Accession AF281308).
 CC
 SQ Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;
 QY Query Match 3.3%; Score 45; DB 23; Length 1350;
 DB Best Local Similarity 100.0%; Pred. No. 1.5e-10; Indels 0; Gaps 0;
 Matches 45; Conservative 0; Mismatches 0;
 292 TCGTCATCGTCACCTGTGCGCCATCAGCCTGACCGCTACTGG 336
 355 TCGTCATCGTCACCTGTGCGCCATCAGCCTGACCGCTACTGG 399

ID AA199918 standard; DNA; 1350 BP.
 XX
 AC AA199918;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Human alpha-2AAR variant encoding DNA.
 XX
 KM Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KM polymorphic site; allelic variant; cardiovascular disease;
 KM central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KM phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1353
 FT /tag= a
 FT /product= "alpha-2AAR"
 FT replace(753,C)
 FT allele
 XX
 PN WO200179561-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US12575.
 XX
 PR 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 XX
 PS WPI: 2001-611728/70.
 DR P-PSDB; AAM52123.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Disclosure; Page 152; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (999GCG99GCG) or (B) (999GCGCTGAG) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2AAR variant
 CC gene.
 SQ Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;

Query Match 3.3%; Score 45; DB 23; Length 1350;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 292 TCGTCATCGTCGACCTGTGCGCATCAGCTGAGACCGCTACTGG 336
 Db 355 TCGTCATCGTCGACCTGTGCGCATCAGCTGAGACCGCTACTGG 399

RESULT 15

ACAS6582
 ID ACH56582 standard; cDNA; 3604 BP.

AC ACH56582;

DT 06-JUN-2003 (first entry)

DE Human signalling pathway polynucleotide probe SEQ ID NO 1180.

XX Human; probe; 86; array element; Parkinson's disease;

KM signalling pathway population; cancer; adenocarcinoma; leukaemia;

KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

OS Homo sapiens.

PN US6500938-B1.

PD 31-DEC-2002.

PF 30-JAN-1998; 98US-0016434.

PR 30-JAN-1998; 98US-0016434.

PA (INCY-) INCYTE GENOMICS INC.

PI Au-Young J, Sellhammer JJ;

DR WPI; 2003-352189/33.

PT Combination of polynucleotide probes, useful as array elements in a

PT microarray for monitoring the expression of a number of target

PT polynucleotides

XX

PS Claim 1; SEQ ID NO 1180; 65pp; English.

XX The invention relates to a combination which, comprises a number of

CC polynucleotide probes comprising a sequence selected from one of the 1490

CC sequences mentioned in the specification. The combination is useful as an

CC array element in a microarray for monitoring the expression of a number

CC of target polynucleotides. The microarray is particularly useful in the

CC diagnosis and treatment of cancer and immunopathology and neuropathology.

CC The microarray is useful in diagnostic and treatment regimens, drug

CC discovery and development, toxicological and carcinogenicity studies,

CC forensics and pharmacogenomics. The microarray is also useful for

CC monitoring progression of diseases and for developing sophisticated

CC profiles for the effects of currently available therapeutic drugs. The

CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs

CC and genomic fragments and in research and diagnostic applications. The

CC array can detect changes in expression in a large number of genes coding

CC for different signalling pathway populations which can be used to diagnose

CC various diseases including cancer e.g. adenocarcinoma and leukaemia,

CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease

CC and Parkinson's disease. The present sequence represents a polynucleotide

CC probe of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format directly from USPTO

CC at seqdata.uspto.gov/sequence.html?docID=06500938B1.

CC

XX

SO Sequence 3604 BP; 555 A; 1272 C; 1134 G; 643 T; 0 other;

Query Match 3.3%; Score 45; DB 25; Length 3604;

Best Local Similarity 100.0%; Pred. No. 1.5e-10;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 292 TCGTCATCGTCGACCTGTGCGCATCAGCTGAGACCGCTACTGG 336
 Db 2432 TCGTCATCGTCGACCTGTGCGCATCAGCTGAGACCGCTACTGG 2476

Search completed: February 8, 2004, 01:59:40
 Job time : 397.679 secs

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953 TTCTTTGCTCCTTGCCCTCATGATCCTTGCTACTGCGCATCTACCTGATGCCAA 101

QY	601	CGCAGCAACCGCAGAGGTCCCGAGGCCACAGGGGGGGGCTTGGGCAGGGGTAGATCCCAACAG	660
Db	1013	CGCAGCAACCGCAGAGGTCCCGAGGCCACAGGGGGGGGCTTGGGCAGGGGTAGATCCCAACAG	1072
QY	661	CCCCGACCCGACATGTGTGGGGCTTTGGCCTCAGGCCAACTGSCCAGCCCTTGCTGTG	720
Db	1073	CCCCCACCAGACCATGTGTGGGGCTTTGGCCTCAGGCCAACTGSCCAGCCCTTGCTGTG	1132
QY	721	GCTTTCGCAGAGAGTCAACGGAACACTCGAAGTCACCTGGGAGAGAGAGAGAGGGGGAG	780
Db	1133	GCTTTCGCAGAGAGTCAACGGAACACTCGAAGTCACCTGGGAGAGAGAGAGAGAGGGGGAG	1192
QY	781	ACCCCTGAAGATATCTGGGACCCGGGCTTTGGCCACCCAGCTTGGGGCGGCCCTTCCCACTCA	840
Db	1193	ACCCCTGAAGATATCTGGGACCCGGGCTTTGGCCACCCAGCTTGGGGCTGCCCTTCCCACTCA	1252
QY	841	GGCCAGGGCCAAAGAGGGGTGTTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG	900
Db	1253	GGCCAGGGCCAAAGAGGGGTGTTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG	1312
QY	901	GA 902	
Db	1313	GA 1314	

RESULT 2
 US-09-016-434-1180
 Sequence 1180, Application US/09016434
 Patent No. 6500938
 GENERAL INFORMATION:
 APPLICANT: Janice Au-Young
 APPLICANT: Jeffrey J. Seilhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,434
 FILING DATE: HEREMITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEO ID NO.: 1180:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3604 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 9176195
 US-09-016-434-1180

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Query Match      3.3%; Score 45; DB 4; Length 3604;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      292 TCGTCATCTGCGCACTGTGGCCATCAGCTGACCGCTACTGCG 336
          |||||
DB       2432 TCGTCATCTGCGCACTGTGGCCATCAGCTGACCGCTACTGCG 2476

```

RESULT 3
 US-09-016-434-1256
 Sequence 1256, Application US/09016434
 Patent No. 6500938
 GENERAL INFORMATION:
 APPLICANT: Janice Au-Young
 APPLICANT: Jeffrey J. Sellhammer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 FORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016.434
 FILING DATE: HERewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1256:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1382 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g219405
 US-09-016-434-1256

	Query Match	2.9%	Score 39	DB 4	length 1382
	Best Local Similarity	100.0%	Pred. No. 2,6e+08		
	Matches 39	Conservative	0	Mismatches 0	Indels 0
Qy	1132	GTGCTCTGCTGGTTCCTTCCTTCGTCAGCAGACGCTG	1170		
Db	1164	GTGCTCTGCTGGTTCCTTCCTTCGTCAGCAGACGCTG	1202		

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Job time : 89.703 secs
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US-09-016-434-1180

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2004, 01:25:52 ; Search time 313.58 Seconds
(without alignments)
10491.225 Million cell updates/sec

Title: US-09-692-077D-2

Perfect score: 1344
Sequence: 1 atgaccaccagagaccctca.....ggaccacagcgctgctga 1344

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 1215238056 residues

Word size : 30

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST.*
1: em_estda:*
2: em_esthm:*
3: em_estln:*
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6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_g88_hum:*
18: em_g88_inv:*
19: em_g88_pln:*
20: em_g88_vrt:*
21: em_g88_fun:*
22: em_g88_man:*
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24: em_g88_pro:*
25: em_g88_rtd:*
26: em_g88_phg:*
27: em_g88_vtl:*
28: gb_g881:*
29: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	28.6	1044	13	BQ880026 AGENCOURT
2	47	3.5	551	9	A1169366 EST215210
3	47	3.5	731	14	CAS11027 UT-R-FJD-
4	45	3.3	2410	11	BC035047 Homo sapi

5	44	3.3	893	12	BI459381
6	41	3.1	872	29	ECAA2BAR
7	39	2.9	301	14	T39448
8	39	2.9	978	13	BUS39106
9	39	2.9	1031	13	BUS38114
10	39	2.9	1176	9	AL549866
11	39	2.9	1201	9	AL573897
12	38	2.8	988	13	BQ887729
13	34	2.5	683	12	BGA30756
14	34	2.5	855	29	GCAG2AAR
15	34	2.5	960	13	BUS38113
16	34	2.5	967	29	CNS03THX
17	33	2.5	451	9	AI461341
18	33	2.5	860	29	CNS03HKO
19	32	2.4	350	10	BE648878
20	32	2.4	723	12	BUS16840
21	32	2.4	761	14	CB952602
22	32	2.4	3594	11	AK046802
23	31	2.3	251	10	BB603339
24	30	2.2	753	13	BUS289357
25	30	2.2	836	13	BU473325
26	30	2.2	1080	29	CC240340

ALIGNMENTS

RESULT 1
BQ880026 1044 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT 8113358 Lupski dorsal root ganglion Homo sapiens cDNA
DEFINITION clone IMAGE:6179035 5', mRNA sequence.
ACCESSION BQ880026
VERSION BQ880026.1 GI:22272034
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1044)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: L1AM13559 row: 1 column: 20
High quality sequence stop: 430.

FEATURES

source

1. 1044
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6179035"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming:
Directionally cloned using the following adaptors:
5'-TCACCCACGCGTCG-3' and
5'-GACTACTTCAGATCGGACGCGCCCTT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dfr)18 tail. The sequence tag for this library is CATCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)"

BASE COUNT 128 a 217 c 163 g 223 t

Query Match 3.5%; Score 47; DB 14; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 CATGGCTCTTCAGTCTCTCTGTGATGGGCTACTGCAACGCTC 1250
DB 42 CATGGCTCTTCAGTCTCTCTGTGATGGGCTACTGCAACGCTC 88

RESULT 4 BC035047 2410 bp mRNA linear HTC 23-SEP-2002
LOCUS BC035047
DEFINITION Homo sapiens, similar to adrenergic, alpha-2A-, receptor, clone
IMAGE:5266354, mRNA.
ACCESSION BC035047
VERSION BC035047.1 GI:23272892
KEYWORDS HTC.
SOURCE Homo sapiens (human)

REFERENCE 1 (bases 1 to 2410)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Strausberg, R.
JOURNAL Direct Submission

Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
REMARK COMMENT
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshitaki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
Contact: amadansystemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 73 Row: 0 Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15718669
This clone has the following problem: frame shifted.

Location/Qualifiers

FEATURES

source

1. 2410
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5266354"
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"

BASE COUNT 406 a 813 c 721 g 470 t

Query Match 3.3%; Score 45; DB 11; Length 2410;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCGTCATCGTGACCTGTGGCCATCAGCGCTGAGCGTACTG 336
DB 568 TCGTCATCGTGACCTGTGGCCATCAGCGCTGAGCGTACTG 612

RESULT 5 B1459381 893 bp mRNA linear EST 21-AUG-2001
LOCUS B1459381
DEFINITION 603200147F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266354 5',
mRNA sequence.
ACCESSION B1459381
VERSION B1459381.1 GI:15250037
KEYWORDS EST.
SOURCE Homo sapiens (human)

REFERENCE 1 (bases 1 to 893)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Strausberg, R.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshitaki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM11671 row: m column: 11
High quality sequence stop: 716.

FEATURES

source

1. 893
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5266354"
/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcagag); Oligo-dT primed using primer 5'-TTTTTTTTTTTVA-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 149 a 303 c 290 g 151 t

Query Match 3.3%; Score 44; DB 12; Length 893;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 CGTCATCGTGACCTGTGGCCATCAGCGCTGAGCGTACTG 336
DB 574 CGTCATCGTGACCTGTGGCCATCAGCGCTGAGCGTACTG 617

RESULT 6 EC042BAR 872 bp DNA linear GSS 14-SEP-2001
LOCUS EC042BAR
DEFINITION Horse alpha2 adrenergic receptor gene fragment probably subtype b,
Genomic survey sequence.
ACCESSION AL606560
VERSION AL606560.1 GI:15591917
KEYWORDS GSS; Alpha2 adrenergic receptor gene.
SOURCE Equus caballus (horse)

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/clone lib="Stratagene placenta #931225"
/note="Organ: placenta; Vector: pBluescript SK-, Site 1:
EcoRI, Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGACG 3' -3'
adaptor sequence: 5' CTCGACTTTTTTTTTTTT 3'"

BASE COUNT      40 a      107 c      71 g      83 t
ORIGIN

Query Match          2.9%; Score 39; DB 14; Length 301;
Best Local Similarity 100.0%; Freq. No. 6,-2e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1132 GTGCTGTGCTGATTCCCTTTCTTTTACGACACCGCTG 1170
|||||
|||||

Db      114 GTGCTGTGCTGATTCCCTTTCTTTTACGACACCGCTG 152
|||||
|||||

RESULT 8
B0539106      978 bp      mRNA      linear      EST 13-SEP-2002
LOCUS
DEFINITION
AGENCOURT 10215036 NIH_MGC_107 Homo sapiens CDNA clone
IMAGE:6568764 5', mRNA_sequence.
ACCESSION
B0539106
VERSION
B0539106.1 GI:22849547
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 978)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: gcgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2757 row: j column: 04
High quality sequence stop: 554.
Location/Qualifiers
1. 978
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6569764"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACTGAG(G). Library constructed by
Ling Hong in the Laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT      223 a      278 c      303 g      174 t
ORIGIN

Query Match          2.9%; Score 39; DB 13; Length 978;
Best Local Similarity 100.0%; Pred. No. 7,-7e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1132 GTGCTGTGCTGATTCCCTTTCTTTTACGACACCGCTG 1170
|||||
|||||

Db      12 GTGCTGTGCTGATTCCCTTTCTTTTACGACACCGCTG 50
|||||
|||||
```

RESULT 9
BUS38114 1031 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT 10186636 NIH_MGC_107 Homo sapiens cDNA clone
IMAGE:6586828 5', mRNA sequence.
ACCESSION BUS38114
VERSION BUS38114.1 GI:22848555
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1031)
NIH-MGC <http://imgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://imgc.lnl.gov>
Plate: LICM2754 row: j column: 20
High quality sequence, stop: 529.
Location/Qualifiers
1. 1031
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6586828"
/issue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_idb="NIH MGC 107"
/note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT 221 a 275 c 330 g 191 t 14 others
ORIGIN
Query Match 2.9%; Score 39; DB 13; Length 1031;
Best Local Similarity 100.0%; Pred. No. 7.8e-07; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1132 GTGCTGTGCTGTTCCCTTCTTTCAGCTACAGCCTG 1170
|||||
DB 12 GTGCTGTGCTGTTCCCTTCTTTCAGCTACAGCCTG 50
|||||
RESULT 10
AL549866 1176 bp mRNA linear EST 31-MAY-2003
LOCUS AL549866 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1054YH02 5-PRIME, mRNA sequence.
ACCESSION AL549866
VERSION AL549866.2 GI:31271684
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1176)
Ling Hong, Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
JOURNAL Unpublished

COMMENT On Feb 15, 2001 this sequence version replaced gi:12886265.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0D1054D010P1.
Location/Qualifiers
1. 1176
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1054YH02"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_idb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 194 a 338 c 425 g 174 t 45 others
ORIGIN
Query Match 2.9%; Score 39; DB 9; Length 1176;
Best Local Similarity 100.0%; Pred. No. 8e-07; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1132 GTGCTGTGCTGTTCCCTTCTTTCAGCTACAGCCTG 1170
|||||
DB 552 GTGCTGTGCTGTTCCCTTCTTTCAGCTACAGCCTG 590
|||||
RESULT 11
AL573897 1201 bp mRNA linear EST 31-MAY-2003
LOCUS AL573897 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1054YH02 3-PRIME, mRNA sequence.
ACCESSION AL573897
VERSION AL573897.2 GI:31295233
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
Ling Hong, Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12933576.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0D1054D010P1.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1054YH02"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_idb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 193 a 391 c 364 g 205 t 48 others
ORIGIN

Query Match 2.9%; Score 39; DB 9; Length 1201;
Best Local Similarity 100.0%; Pred. No. 8e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 GTGCTGCGGTTCCCTCTCTCTGAGTACAGCTG 1170
|||||
DB 733 GTGCTGCGGTTCCCTCTCTCTGAGTACAGCTG 695

RESULT 12
B0887729 988 bp mRNA linear EST 16-AUG-2002
LOCUS B0887729
DEFINITION AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
5', mRNA sequence.
ACCESSION B0887729
VERSION B0887729.1 GI:22279743
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/.
1 (bases 1 to 988)
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgabbs-remail.nih.gov
COMMENT Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: Resgen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM13739 row: m column: 06
High quality sequence start: 8
High quality sequence stop: 509.
Location/Qualifiers
1..988
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6313133"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_129"
/note="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.cdb; Site 1: EcoRV; Site 2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this
is a NIH_MGC library."

BASE COUNT 158 a 349 c 300 g 181 t
ORIGIN

Query Match 2.8%; Score 38; DB 13; Length 988;
Best Local Similarity 100.0%; Pred. No. 2.2e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 GACGTCCTCTGCACTCTGCTGACCTGCTG 311
|||||
DB 188 GACGTCCTCTGCACTCTGCTGACCTGCTG 225

RESULT 13
B0830756 683 bp mRNA linear EST 22-MAY-2001
LOCUS B0830756
DEFINITION 602767450F1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:4909381 5',
mRNA sequence.
ACCESSION B0830756
VERSION B0830756.1 GI:14178343
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 683)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1817 row: c column: 14
High quality sequence stop: 677.
Location/Qualifiers
1..683
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4909381"
/issue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_42"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(C). Size-selected for
average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library. |"

BASE COUNT 122 a 202 c 235 g 124 t
ORIGIN

Query Match 2.5%; Score 34; DB 12; Length 683;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 AGTTCTTCTTGATCGGCTACTGCAACGCTC 1250
|||||
DB 100 AGTTCTTCTTGATCGGCTACTGCAACGCTC 133

RESULT 14
GGA42AAR 855 bp DNA linear GSS 14-SEP-2001
LOCUS GGA42AAR
DEFINITION Chicken alpha2 adrenergic receptor gene fragment probably subtype
a, genomic survey sequence.
ACCESSION AL606540
VERSION AL606540.1 GI:15591915
KEYWORDS GSS; Alpha2 adrenergic receptor gene.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 855)
Hunter, C. and Elgar, G.
Alpha2 adrenergic receptor gene
Unpublished
2 (bases 1 to 855)
Hunter, C.
Direct Submission
Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB, UK Email:
bichep@hmp.mrc.ac.uk
Location/Qualifiers
1..855
/organism="Gallus gallus"
/mol_type="genomic DNA"

BASE COUNT 201 a 248 c 245 g 161 t
ORIGIN /db_xref="taxon:9031"

Query Match 2.5%; Score 34; DB 29; Length 855;
Best Local Similarity 100.0%; Pred.No. 0.00016;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 CAAGCCACCCCGCCGATCAAGTCATCATC 399
DB 144 CAAGCCACCCCGCCGATCAAGTCATCATC 177

RESULT 15
BUS38113 960 bp mRNA linear EST 13-SEP-2002
LOCUS AGENCOURT 10186620 NIH_MGC_107 Homo sapiens cDNA clone
DEFINITION IMAGE:6568627 5', mRNA sequence.
ACCESSION BUS38113
VERSION BUS38113.1 GI:22848554
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 960)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LCM2754 row: j column: 19
High quality sequence start: 46
High quality sequence stop: 558.
Location/Qualifiers

FEATURES
source
1..960
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6568627"
/cissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 107"
/note="Organ: breast; Vector: pORF7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 214 a 268 c 294 g 184 t
ORIGIN

Query Match 2.5%; Score 34; DB 13; Length 960;
Best Local Similarity 100.0%; Pred.No. 0.00016;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 AGTTCTTCTTGATCGGCTACTGCAACAGCTC 1250
DB 97 AGTTCTTCTTGATCGGCTACTGCAACAGCTC 130

Search completed: February 8, 2004, 06:35:53
Job time : 3115.58 secs

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variation	/gene="ADRA2B"	
	/note="compared to wild type sequence presented in GenBank Accession Number AF005900; polymorphic sequence lacks three glu residues at this location"	
	/frequency="Caucasians 0.31; African-Americans 0.12"	
	/replace="gaagaagag"	
BASE COUNT	220 a 458 c 400 g 266 t	
ORIGIN		
Query Match	100.0%; Score 1344; DB 9; Length 1344;	
Best Local Similarity	100.0%; Pred. No. 7e-216;	
Matches 1344; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 ATGAGCACACGAGGACCCTACTCCGTGGAAGGCCACAGGGGCATAGGGGGCCATACC 60	
Dd	1 ATGAGCACACGAGACCCCTACTCGTGAGGCGACAGGGGCATAGCGGGCCATACCC 60	
Oy	61 TTCTCATTTCTTTACCATCTTGCGGACGCTCTGTATCTTGCTGTGTGACAGC 120	
Dd	61 TTCCTATTCTTTACCATCTTTGGGACAAGCCTCTGTATCTTGCTGTGTGACAGC 120	
Oy	121 CGCTCGCTGGCGGCCCTTCAGAAGCTGTTCTGTGTGTGCTGGCGCGCCGCGACATCTG 180	
Dd	121 CGCTCGCTGGCGGCCCTTCAGAAGCTGTTCTGTGTGTGCTGGCGCGCCGCGACATCTG 180	
Oy	181 GTGGCGACGCTCATCATCCTTTCTCGCTGGCGAACAGAGCTGCGGGCTACTGTGAACCTTC 240	
Dd	181 GTGGCGACGCTCATCATCCTTTCTCGCTGGCGAACAGAGCTGCGGGCTACTGTGAACCTTC 240	
Oy	241 CGGCGCAAGTGATGAGGTATCCTTGCGCTGACCGTCAAGTCTTTCTGCACTCTGTTCATC 300	
Dd	241 CGGCGCAAGTGATGAGGTATCCTTGCGCTGACCGTCAAGTCTTTCTGCACTCTGTTCATC 300	
Oy	301 GTGCACTGTGCGGCATATAGCTTGAACCGCTACTGAGCGCTGTAGCGCGCGCTGTGAATAC 360	
Dd	301 GTGCACTGTGCGGCATATAGCTTGAACCGCTACTGAGCGCGCTGTGAATAC 360	
Oy	361 AACTCCAAGGACACCCCGCGCGCGATCAAGTGACATCTTCACGTGTGGCTCATGGCC 420	
Dd	361 AACTCCAAGGACACCCCGCGCGCGATCAAGTGACATCTTCACGTGTGGCTCATGGCC 420	
Oy	421 GCCGTATCTGTGCTGCGGCCCTTCATATCTTAACAAGGGCGACACAGGGCCCCCAGCGCGGG 480	
Dd	421 GCCGTATCTGTGCTGCGGCCCTTCATATCTTAACAAGGGCGACACAGGGCCCCCAGCGCGGG 480	
Oy	481 CGCCCCCAGTGAAGCTCAACAGAGAGCGCTGTATCATCTTGCGCTCCAGCATGGATCT 540	
Dd	481 CGCCCCCAGTGAAGCTCAACAGAGAGCGCTGTATCATCTTGCGCTCCAGCATGGATCT 540	
Oy	541 TTTCTTTGCTCTTGAGCTCATCATGATCCTTGTCTACCTGCGCATCTACCTGATGGCCAAA 600	
Dd	541 TTTCTTTGCTCTTGAGCTCATCATGATCCTTGTCTACCTGCGCATCTACCTGATGGCCAAA 600	
Oy	601 CGAGCAAACGCGCAGAGGTCCAGGGGCCAAGGGGGGGGCTGTGGAGAGGTGATCCAAAGAG 660	
Dd	601 CGAGCAAACGCGCAGAGGTCCAGGGGCCAAGGGGGGGGCTGTGGAGAGGTGATCCAAAGAG 660	
Oy	661 CCCCGACCCGACCATGTGTGGGGCTTTGGCTTCACGCCAAATCTGCCAGCCCTGTGTGTG 720	
Dd	661 CCCCGACCCGACCATGTGTGGGGCTTTGGCTTCACGCCAAATCTGCCAGCCCTGTGTGTG 720	

QY	721	GCTTCTGCAAGAGGTCAACGAGCACTCGAAGTCACTGGGAGAAAGAGAGGGAG	780
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Db	721	GCTTCTGCAAGAGGTCAACGAGCACTCGAAGTCACTGGGAGAAAGAGAGGGAG	780
QY	781	ACCCCTGAAGTACTGGGACCCGGGCTTTGGCCACCAGTTGGCTCCCTTCCCACTCA	840
QY	781	ACCCCTGAAGTACTGGGACCCGGGCTTTGGCCACCAGTTGGCTCCCTTCCCACTCA	840
Db	781	ACCCCTGAAGTACTGGGACCCGGGCTTTGGCCACCAGTTGGCTCCCTTCCCACTCA	840
QY	841	GGCCAGGGCCGAAAGAGAGGTTGTTGGGCACTCTCCAGAGATGAAGCTGAAAGAG	900
QY	841	GGCCAGGGCCGAAAGAGAGGTTGTTGGGCACTCTCCAGAGATGAAGCTGAAAGAG	900
Db	841	GGCCAGGGCCGAAAGAGAGGTTGTTGGGCACTCTCCAGAGATGAAGCTGAAAGAG	900
QY	901	GAGGAGGAGAGAGAGTGTGAACCCGAGGCAAGGACAGTGTCTCCGGCCCTCAGCTTGC	960
QY	901	GAGGAGGAGAGAGAGTGTGAACCCGAGGCAAGGACAGTGTCTCCGGCCCTCAGCTTGC	960
Db	901	GAGGAGGAGAGAGAGTGTGAACCCGAGGCAAGGACAGTGTCTCCGGCCCTCAGCTTGC	960
QY	961	AGCCCCCGCTGACAGACGCAAGGAGCTCCGGGCTGCGCACTTACGTGGCCAGGTG	1020
QY	961	AGCCCCCGCTGACAGACGCAAGGAGCTCCGGGCTGCGCACTTACGTGGCCAGGTG	1020
Db	961	AGCCCCCGCTGACAGACGCAAGGAGCTCCGGGCTGCGCACTTACGTGGCCAGGTG	1020
QY	1021	CTCCTGGGCAAGGAGGCTGAGTGTGCTAATAGTGGGCAAGTGTGGCTGCAAGGGCGACGTG	1080
QY	1021	CTCCTGGGCAAGGAGGCTGAGTGTGCTAATAGTGGGCAAGTGTGGCTGCAAGGGCGACGTG	1080
Db	1021	CTCCTGGGCAAGGAGGCTGAGTGTGCTAATAGTGGGCAAGTGTGGCTGCAAGGGCGACGTG	1080
QY	1081	ACCCGGAGAGAGCCCTTCAACCTGTGTGGCTGTGTGATTTGCTGTGC	1140
QY	1081	ACCCGGAGAGAGCCCTTCAACCTGTGTGGCTGTGTGATTTGCTGTGC	1140
Db	1081	ACCCGGAGAGAGCCCTTCAACCTGTGTGGCTGTGTGATTTGCTGTGC	1140
QY	1141	TGTTTCCCTCTCTTTCAGCTACAGCTGAGGCGCATCTGCCGAGACATGCAAGGTG	1200
QY	1141	TGTTTCCCTCTCTTTCAGCTACAGCTGAGGCGCATCTGCCGAGACATGCAAGGTG	1200
Db	1141	TGTTTCCCTCTCTTTCAGCTACAGCTGAGGCGCATCTGCCGAGACATGCAAGGTG	1200
QY	1201	CCCCATGGCCCTTTCAGCTTCTTTCAGTGTGGCTGCTGCAACAGCTCACTGAACCT	1260
QY	1201	CCCCATGGCCCTTTCAGCTTCTTTCAGTGTGGCTGCTGCAACAGCTCACTGAACCT	1260
Db	1201	CCCCATGGCCCTTTCAGCTTCTTTCAGTGTGGCTGCTGCAACAGCTCACTGAACCT	1260
QY	1261	GTTATCTTACACCATCTTTCACAGAGACTTCGGCCGCTGCTTCCGAGAGATCTGTGCGC	1320
QY	1261	GTTATCTTACACCATCTTTCACAGAGACTTCGGCCGCTGCTTCCGAGAGATCTGTGCGC	1320
Db	1261	GTTATCTTACACCATCTTTCACAGAGACTTCGGCCGCTGCTTCCGAGAGATCTGTGCGC	1320
QY	1321	CCGTGAGACCCAGACGGCTGTGA	1344
QY	1321	CCGTGAGACCCAGACGGCTGTGA	1344
Db	1321	CCGTGAGACCCAGACGGCTGTGA	1344
RESULT 3			
AC092603/c			
LOCUS	AC092603	22842 bp	DNA linear PRI 01-MAR-2002
DEFINITION	Homo sapiens BAC clone Rpl1-1396 from 2, complete sequence.		
ACCESSION	AC092603	AC073396	
VERSION	AC092603.2	GI:1630539	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 22842)		
TITLE	Sullivan, J.E. and Waterston, R.		
JOURNAL	Toward a complete human genome sequence		
EDLINE	Genome Res. 8 (11), 1097-1108 (1998)		
PUBMED	99063792		
REFERENCE	9847074		
TITLE	2 (bases 1 to 22842)		
AUTHORS	Matlinka, S., Abbott, A., Hawkins, M., Elliott, G. and Doeber, A.		
JOURNAL	The sequence of Homo sapiens BAC clone Rpl1-1396		
EDLINE	Unpublished (2001)		
REFERENCE	3 (bases 1 to 22842)		
AUTHORS	Waterston, R.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-JUN-2001) Genome Sequencing Center, Washington		
EDLINE	University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA		
REFERENCE	4 (bases 1 to 22842)		

AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (20-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE
 TITLE 5 (bases 1 to 22842)
 JOURNAL Waterston, R.H.
 Direct Submission
 Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE
 TITLE 6 (bases 1 to 22842)
 JOURNAL Waterston, R.H.
 Direct Submission
 Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Oct 20, 2001 this sequence version replaced gi:14916188.

COMMENT

 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: saplens@wustl.wustl.edu

 Summary Statistics
 Center project name: H_NH0139J06
 Drafting Center: MIBR_NH0139J06

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
 The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Caranese, J.V. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-401C13, 2000 bp overlap; the clone sequenced to the right is RP11-574017, 2000 bp overlap. Actual end of this clone is at base position 48999 of RP11-574017. Polymorphisms have been identified between AC013272 and AC092603.

FEATURES
 Source The sequence of AC073396 has been incorporated into AC092603.
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repeat_region      1665..1966
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repeat_region      3183..3448
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repeat_region      5541..5566
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repeat_region      6195..6301
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Best Local Similarity 99.3%; Pred. No. 1.6e-215;
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DB      15090 CGGCGCAGTGTGTGAGGTGATCTGAGCGCTCGACGCTCTTCTGACCTCGTCCATC 15031
QY      301 GTGCACCTGTGCGGCATCAGCTGAGCGCTACTGTGAGCGCGCGCGCTGAGATAC 360
DB      15030 GTGCACCTGTGCGGCATCAGCTGAGCGCTACTGTGAGCGCGCGCGCTGAGATAC 14971
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DB      14970 AACTTCGAAGGCAAGCGCGCGCGCGCATCAAGTGTATCTCTCACTGTGTGCTCATGCC 14911
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DB      14910 GCCGTATCTCGTGGCGCGCCCTCATCATCAAGGGCGCAAGGGCGCGCGCGGG 14851
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QY      601 CGGAGCAACGCGAGAGTCCAGGGGCGGAGGGGGGCTGGGCGAGGGTGAATCCAAACAG 660
DB      14730 CGGAGCAACGCGAGAGTCCAGGGGCGGAGGGGGGCTGGGCGAGGGTGAATCCAAACAG 14671
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QY      721 GCTTCTCCAGAGAGTCAACGACACTCGAAGTCCACTGGGAGAGAGAGAGAGGAG 780
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QY      781 ACCCTGAAGATCTGGAACCCGGGCTTGACCCAGTGTGGCTCTTCCCACTCA 840
DB      14550 ACCCTGAAGATCTGGAACCCGGGCTTGACCCAGTGTGGCTCTTCCCACTCA 14491
QY      841 GGCCAGGCGCAAGAGAGGCTTTTGTGGGCACTTCCAGATGGAAGTGAAGAGAG 900
DB      14490 GGCCAGGCGCAAGAGAGGCTTTTGTGGGCACTTCCAGATGGAAGTGAAGAGAG 14431
QY      901 GAGAGAGAGAGAGAGTGTGAACCCAGGAGTGCAGTGTCTCGGCTCAGTTGC 960
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QY      1021 CTCTGGGCGAGGGGCTGTGCTATATGATGAGGCAATGTGTGCGTCCAGAGGCGACTG 1080
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QY      1081 ACCCGGAGAGAGGCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB      14250 ACCCGGAGAGAGGCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14191
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QY      1321 CCGTGACCCAGAGCGGCTGTGA 1344
DB      14010 CCGTGACCCAGAGCGGCTGTGA 13987

RESULT 4
AX350489
LOCUS      AX350489 1353 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 1 from Patent WO0179561.
ACCESSION  AX350489
VERSION    AX350489.1 GI:18616091
KEYWORDS
SOURCE
ORGANISM  Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Liggett, S.B. and Small, K.M.
  Alpha-2 adrenergic receptor polymorphisms
  Patent: WO 0179561-A 1 25-Oct-2001;
  Liggett, Stephen B. (US) ; Small, Kersten M. (US)
FEATURES
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            1..1353
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            /mol_type="genomic DNA"
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BASE COUNT      224 a 458 c 405 g 266 t
ORIGIN
Query Match      98.6%; Score 1325; DB 6; Length 1353;
Best Local Similarity 99.3%; Pred. No. 1.1e-212;
Matches 1344; Conservative 0; Mismatches 0; Indels 9; Gaps 1;
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QY	61	TTCTCTCATTTCTTTACATCTTCCGCAACGCTCTGTATCTGTGGCTGTGTGACAGC	120
Db	61	TTCTCTCATTTCTTTACATCTTCCGCAACGCTCTGTATCTGTGGCTGTGTGACAGC	120
QY	121	CGCTCGTGGCGCCCTTGAGACCTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	180
Db	121	CGCTCGTGGCGCCCTTGAGACCTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	180
QY	181	GTGGCCACGCTCATCATCCCTTTCTCGTGGCAACAGAGCTGTGGGCTACTGGTACTTC	240
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QY	241	CGGCGCAGTGGGAGGAGGTGAACCTGGGCGCTGCAAGTGTCTTTGTGACCTGTGCATC	300
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QY	301	GTGACACTGTGGCCATCAGCCTGAGCCGCTACTGGGCGGTGACCGCGGCTGTGAGTAC	360
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QY	895	---GAGGAG	900
Db	901	GAGGAG	951
QY	951	TCAGCTTGCAG	960
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Qy      895  --GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1312
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RESULT 7
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 HUMADRA2RA
 Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
 M34041.1 GI:178197

KEYWORDS
 alpha-2-adrenergic receptor; plasma membrane protein;
 receptor-coupled G protein.
SOURCE
 Homo sapiens (human)
ORGANISM
 Homo sapiens
REFERENCE
 1 (bases 1 to 2072)
 Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W.,
 Yang, F., T.L., Caron, M.G., and Lefkowitz, R.J.
 Expansion of the alpha 2-adrenergic receptor family: cloning and
 characterization of a human alpha 2-adrenergic receptor subtype,
 Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
 90311349
JOURNAL
 MEDLINE
 PUBMED
 2164221
COMMENT
 Original source text: Human placenta DNA, clone alpha-2 c2.
 Draft entry and computer-readable sequence for (1) kindly submitted
 by J.W.Lomasney, 03-MAY-1990, for release after publication.
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 VLATLROGLVIGRGVAGISQWWRRAHTRREKRFYLAIVIGVFLCWPFPSYS
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Query Match
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 Db 413 ATGACACACAGAGACCCCTACTCCGTCAGGCGACAGCGGCCCATAGCGGCGCATCAC 472
 Qy 61 TTCTGATCTCTTTTACATCTTTCGCAACGCTGTGTCATCTGCGCTGTGTTACACAGC 120
 Db 473 TTCTGATCTCTTTTACATCTTTCGCAACGCTGTGTCATCTGCGCTGTGTTACACAGC 532
 Qy 121 CGCTGCTGCGGCGCCCTCAGAACCTGTCCTGTGTGCTGCGCGCGCGCAATCTCTG 180
 Db 533 CGCTGCTGCGGCGCCCTCAGAACCTGTCCTGTGTGCTGCGCGCGCGCAATCTCTG 592
 Qy 181 GTGGCAGAGCTCATCATCTCTTTCGTCGCGCAACAGAGTGTGGAGCTACAGTACTTC 240
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 Qy 301 GTGCACTGTGTCGCGCATCAGCCCTGAGACCGCTACTGTGGCGGTGAGCGCGCTGAGATAC 360
 Db 713 GTGCACTGTGTCGCGCATCAGCCCTGAGACCGCTACTGTGGCGGTGAGCGCGCTGAGATAC 772

QY 361 AACTCAAGCGACCCCGCGCGCATGATGATCATCTCTGATGCTCATGCC 420
DB 773 AACTCAAGCGACCCCGCGCGCATGATGATCATCTCTGATGCTCATGCC 832
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DB 833 GCCGATCTGCTGCGCGCGCGCATGATGATCATCTCTGATGCTCATGCC 892
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DB 893 CGCCCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 952
QY 541 TTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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QY 841 GCGCAGGCGCGCAGAGGTGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCG 894
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QY 895 ---GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 951
DB 1313 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1372
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DB 1373 TCAGCTTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1432
QY 1012 GCGCAGGCTGCTGCTGCGCAGAGGTGCTGCTGCTGCTGCTGCTGCTGCT 1071
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QY 1072 GCGCAGGCTGCTGCTGCGCAGAGGTGCTGCTGCTGCTGCTGCTGCTGCT 1131
DB 1493 GCGCAGGCTGCTGCTGCGCAGAGGTGCTGCTGCTGCTGCTGCTGCTGCT 1552
QY 1132 GTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
DB 1553 GTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1612
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DB 1613 TGCAGAGTGCAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1672
QY 1252 CTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311
DB 1673 CTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1732
QY 1312 CTGTCG 1344
DB 1733 CTGTCG 1765

RESULT 8
AX548756
LOCUS AX548756 3274 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 41 from Patent WO02061087.
ACCESSION AX548756
VERSION AX548756.1 GI:25813686
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Burner, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 41 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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/organism="Homo sapiens"
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BASE COUNT 587 a 979 c 967 g 741 t
ORIGIN
Query Match 98.3%; Score 1321.8; DB 6; Length 3274;
Best Local Similarity 99.2%; Pred. No. 3.3e-212;
Matches 1342; Conservative 0; Mismatches 2; Indels 9; Gaps 1;
QY 1 ATGAGCACCAAGAGCCCTTACTCGGACGAGCCAGCGCGCGCGCGCGCGCG 60
DB 1 ATGAGCACCAAGAGCCCTTACTCGGACGAGCCAGCGCGCGCGCGCGCGCG 60
QY 61 TTCTCTATCTCTTACATCTTCCGCAAGCTCTGATCTCTGATCTCTGATCT 120
DB 61 TTCTCTATCTCTTACATCTTCCGCAAGCTCTGATCTCTGATCTCTGATCT 120
QY 121 CGCTCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CGCTCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GTGGCAGCGCTATCATCTCTTCTGCTGCGCGCGCGCGCGCGCGCGCG 240
DB 181 GTGGCAGCGCTATCATCTCTTCTGCTGCGCGCGCGCGCGCGCGCGCG 240
QY 241 CGGCGCAGCGTGCAGAGGTGCTGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 CGGCGCAGCGTGCAGAGGTGCTGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 GTGCACTGTGCGCATCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 301 GTGCACTGTGCGCATCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 AACTCAAGCGACCCCGCGCGCGCATGATGATCATCTCTGATGCTCATGCC 420
DB 361 AACTCAAGCGACCCCGCGCGCGCATGATGATCATCTCTGATGCTCATGCC 420
QY 421 GCCGATCTGCTGCGCGCGCGCATGATGATCATCTCTGATGCTCATGCC 480
DB 421 GCCGATCTGCTGCGCGCGCGCATGATGATCATCTCTGATGCTCATGCC 480
QY 481 CGCCCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 CGCCCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 TTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 TTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CGCAGCAACCGCAGAGGTCCCAAGGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 601 CGCAGCAACCGCAGAGGTCCCAAGGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 661 CCCGACCCGACCGCAGAGGTCCCAAGGCGCGCGCGCGCGCGCGCGCGCGCG 720

Db 661 CCCGACCCGACATGCTGGGGCTTTGGCTCAGCCAAACTGCCAGCCCTGCTGTG 720
Qy 721 GCTTCTGCAAGAGGTGAACGACACTCGAAGTCCATGGGGAAGAGAGAGAGAGAG 780
Db 721 GCTTCTGCAAGAGGTGAACGACACTCGAAGTCCATGGGGAAGAGAGAGAGAGAG 780
Qy 781 ACCCTGAAGTACTGAGACCCGGGCTTGGCACCCAGTGGGGCTTCCCACTCA 840
Db 781 ACCCTGAAGTACTGAGACCCGGGCTTGGCACCCAGTGGGGCTTCCCACTCA 840
Qy 841 GGGCAGGGCCAG 894
Db 841 GGGCAGGGCCAG 900
Qy 895 ---GAG 951
Db 901 GAG 960
Qy 952 TCAGCTTGCAGACCCCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1011
Db 961 TCAGCTTGCAGACCCCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1012 GGGCAGGTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1071
Db 1021 GGGCAGGTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy 1072 GGGCAGGTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1131
Db 1081 GGGCAGGTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 1132 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1191
Db 1141 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Qy 1192 TGCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251
Db 1201 TGCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Qy 1252 CTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
Db 1261 CTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Qy 1312 CTGTCGCGCCCGTGGAGCCAGACGCGCTGTGA 1344
Db 1321 CTGTCGCGCCCGTGGAGCCAGACGCGCTGTGA 1353

RESULT 9
AY150333 1356 bp mRNA linear MAM 25-NOV-2002
LOCUS Tupaia belangeri alpha-2B adrenoceptor mRNA, complete cds.
DEFINITION AY150333
ACCESSION AY150333.1 GI:25298985
VERSION
KEYWORDS
SOURCE
ORGANISM Tupaia belangeri (tree shrew)
Tupaia belangeri
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Scandentia; Tupaidea;
REFERENCE
1 (bases 1 to 1356)
Heilbronner, U., van Kampen, M., Isovich, E. and Fluegge, G.
Thalamic alpha-2B adrenoceptors under chronic stress: persistent
upregulation in the paraventricular nucleus
Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 1356)
Fluegge, G. and Meyer, H.
Direct Submision
AUTHORS
TITLE Submitted (13-SEP-2002) Neurobiology, German Primate Center (DPZ),
JOURNAL Kellnerweg 4, Goettingen 37077, Germany
FEATURES
source
1..1356
/organism="Tupaia belangeri"
/mol_type="mRNA"
/db_xref="taxon:37347"

CDS
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/protein_id="AA072436.1"
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KOPRPVGRASASAKLPTLASLATGEGNHSKPPGNEDGETPDPGRVLPWSA
ALASSQOKEGVREASABEEBEEBEEBEEBEEBEEBEEBEEBEEBEEBEEBEEB
RVATLRGQVILSRGVGAAGQWRRRAHLTRKRFPLVAVIGVFLCWPFFFSY
SIGALIPROCKVPHGLFQFFFWIYGYNSLIPVITITIPNDPFRARFRLICRWPTQ
W"

BASE COUNT 221 a 471 c 390 g 274 t
ORIGIN

Query Match 84.3%; Score 1132.8; DB 4; Length 1356;
Best Local Similarity 90.9%; Pred. No. 2e-180;
Matches 1232; Conservative 0; Mismatches 112; Indels 12; Gaps 2;

Qy 1 ATGAGACCAAGAGACCCCTAATCTCGTGACAGCCAGCCGACATAGCGGCGCATCAC 60
Db 1 ATGAGTCAACAGAGAGCCCTACTCGTGACAGCCAGCCGCGCATAGCGGCGCATCACT 60
Qy 61 TTCTCAATTTCTTTACATCTTTCGGCAACGCTCTGTATCTCTGCTGTGTGACACAGC 120
Db 61 TTCTCAATTTCTTTACATCTTTCGGCAACGCTCTGTATCTCTGCTGTGTGACACAGC 120
Qy 121 CGCTCGTGGCGCCCTCGAAGACTGTTCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 CGCTCGTGGCGCCCTCGAAGACTGTTCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 180
Qy 181 GTGGCAAGCTGATCATCTCTTTCGTGGCCAGAGCTGTGGCTAATCTGATCTTC 240
Db 181 GTGGCAAGCTGATCATCTCTTTCGTGGCCAGAGCTGTGGCTAATCTGATCTTC 240
Qy 241 CGGCGCAAGTGGTGGAGAGTATCTGCGCTGAGAGTGTCTTTCGACCTGCTGCATC 300
Db 241 CGGCGCAAGTGGTGGAGAGTATCTGCGCTGAGAGTGTCTTTCGACCTGCTGCATC 300
Qy 301 GTGCACTGTGCGCATCATCTGACCGCTATCTGGGCGTGAAGCCGCGCTCGATAC 360
Db 301 GTGCACTGTGCGCATCATCTGACCGCTATCTGGGCGTGAAGCCGCGCTCGATAC 360
Qy 361 AACTCGAAGCGACCCCGCGCGCATCAAGTGCATATCTGATGCTGATCGCC 420
Db 361 AACTCGAAGCGACCCCGCGCGCATCAAGTGCATATCTGATGCTGATCGCA 420
Qy 421 GCGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GCGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 CGCCCCAGTGAAGCTCAACAGAGGCTGTATATCTGTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 CGCCCCAGTGAAGCTCAACAGAGGCTGTATATCTGTGCTGCTGCTGCTGCTGCTGCT 540
Qy 541 TTCTTGTCTCTTCTCATCATGATCTTGTCTACCTGCGCATCTGATGCGCAAA 600
Db 541 TTCTTGTCTCTTCTCATCATGATCTTGTCTACCTGCGCATCTGATGCGCAAA 600
Qy 601 CGAGCAACCGAGAGTCCAGAGCGCAAGGGGGGCTGGAGAGGTAGTCAAGCAG 660
Db 601 CGAGCAACCGAGAGTCCAGAGCGCAAGGGGGGCTGGAGAGGTAGTCAAGCAG 660
Qy 661 CCCGAGCCGACATGATGGGGCTTGGCTGAGCCAACTGCGAGCCCTGGCC---TCT 717
Db 661 CCCGAGCCGATGCTTGGCGGGCTTCAAGCTTCAAGCTTCAAGCTTGGCTTCTT 720
Qy 718 GTGGCTTTCAGAGAGTCAACGACACTCGAAGTCTGAGGAGAGAGAGAGAGAGAG 777

Db 721 CTGGCTACGCGGAGAGGCAATGGGCACTCCAGCCTCTGGGAAAGAGGAGACGG 780
Qy 778 GAGACCCCTGAAAGATCTGGGACCCGGGCTTGGCCACCAGTTGGGCTGCCAAC 837
Db 781 GAGACCCCTGAAAGATCTGGGACCCGGGCTTGGCCACCAGTTGGGCTGCCAAC 840
Qy 838 TCAGGCGAGGCGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 888
Db 841 TCAGGCGAGGCGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Qy 889 GCTGAAG 948
Db 901 GAGGAG 960
Qy 949 GCGCTCAGCTTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1008
Db 961 GCGCTCAGCTTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Qy 1009 GGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1068
Db 1021 GGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Qy 1069 AGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1128
Db 1081 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Qy 1129 TTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
Db 1141 TTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Qy 1189 CACTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1248
Db 1201 CACTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Qy 1249 TCACTGAACCTGTTATCTACATCTTCAACCAAGAGCTTCCGCGCTTCCGAGG 1308
Db 1261 TCACTGAACCTGTTATCTACATCTTCAACCAAGAGCTTCCGCGCTTCCGAGG 1320
Qy 1309 ATCCTGTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1344
Db 1321 ATCCTGTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1356

RESULT 10
CPUS5723 1987 bp DNA linear ROD 05-SEP-2001
LOCUS Cavia porcellus alpha-2B adrenoceptor gene, complete cds.
DEFINITION U55723
ACCESSION U55723.1 GI:818876
VERSION
KEYWORDS
SOURCE
ORGANISM Cavia porcellus (domestic guinea pig)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
1 (bases 1 to 1987)
Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and
Regan,J.W.
Heterologous expression of the cloned guinea pig alpha 2A, alpha
2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and
functional coupling to a CAMP-responsive reporter gene
Biochem. Pharmacol. 51 (3), 291-300 (1996)
JOURNAL MEDLINE
PUBMED 96152573
8573196
2 (bases 1 to 1987)
Richman,J.G.
Direct Submision
Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
AZ 85721, USA
FEATURES
Source
1. 1987
Location/Qualifiers
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/mol_type="genomic DNA"

CDs
/strain="Sasco Hartley albino"
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/clone="GP" alpha-2B"
328..1674
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/protein_id="AA67075.1"
/db_xref="GI:818877"
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PCKIQEAWYIILASSISFAPCLIMILVYLILYIAKSHRGPAPKAGPBGESK
ESRPSGGAASAKVPLPLASITGBANGHPKPTGSEGTSSBDPGATLPPSWA
LPTSGGOKKAVILAPAESEEESEEGECPQAPGLPASMCPSLQOQSRVL
ATIRGOVILGRGVAVDQWWRRTOTREKTRPLVAVIGVFLCWPPFPFTYSIG
AICPHCKVPHSLPQPPFWIGYNSSLNPIYITIFNDFRARRRILCRWQTQAW"

BASE COUNT 318 a 663 c 605 g 401 t
ORIGIN

Query Match 77.8%; Score 1046; DB 10; Length 1987;
Best Local Similarity 87.5%; Pred. No. 6.9e-166;
Matches 1181; Conservative 0; Mismatches 160; Indels 9; Gaps 3;

Qy 1 ATGAGCACCAGAGAGACCCCTTACTCCGTGACAGGCAACAGCGGCATAGCGGCGCCATACC 60
Db 328 ATGAGCACCAGAGAGACCCCTTACTCCGTGACAGGCAACAGCGGCATAGCGGCGGTATACC 387
Qy 61 TTGCTATTTCTTTTACATCTTGGGACAGCTGTGTATCTCTGCTGTGTGACAGC 120
Db 388 TTGCTATTTCTTTTACATCTTGGGACAGCTGTGTATCTCTGCTGTGTGACAGC 447
Qy 121 CGCTCGGTGAGCGCCCTGAGAACTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 448 CGCTCGGTGAGCGCCCTGAGAACTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 507
Qy 448 CGCTCGGTGAGCGCCCTGAGAACTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 507
Db 181 GTGGCAGCGCTATCATCTCTTCTGCTGAGCAACAGCTGTGTGTGTGTGTGTGTGTGTGTGT 240
Qy 508 GTGGCAGCGCTATCATCTCTTCTGCTGAGCAACAGCTGTGTGTGTGTGTGTGTGTGTGTGT 567
Db 241 CGGCGCAGGT 300
Qy 568 TGGCGCAGGT 627
Db 301 GTGACCTGTGAGCGCATACAGCTGAGACCGCTACTGAGGCGGTGAGCGCGCGGTGAGTAC 360
Qy 628 GTGACCTGTGAGCGCATACAGCTGAGACCGCTACTGAGGCGGTGAGCGCGGTGAGTAC 687
Db 361 AACTCCAGGCAACCCCGCGCGCATCAAGTGATCATCTCACTGTGTGTGTGTGTGTGTGTGTGT 420
Qy 688 AACTCCAGGCAACCCCGCGCGCATCAAGTGATCATCTCACTGTGTGTGTGTGTGTGTGTGTGT 747
Db 421 GCGGTATCTGCTGCGCGCGCATCAAGTGATCATCTCACTGTGTGTGTGTGTGTGTGTGTGTGT 480
Qy 748 GCGGTATCTGCTGCGCGCGCATCAAGTGATCATCTCACTGTGTGTGTGTGTGTGTGTGTGTGT 805
Db 481 CGGCGCAGGCAAGCTCAACAGAGGCGGTGTATCTGTGCTTCCAGCATCGATCT 540
Qy 806 -GTCCCGAGTGAAGATCAACAGAGGCGGTGTATCTGTGCTTCCAGCATCGATCT 864
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Qy 865 TTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 924
Db 601 CGAGCAACCGCAGAGGTCCAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy 925 CGAGCAACCGCAGAGGTCCAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 984
Db 661 CCGGCAACCGCAGATGTGGGCTTTGGCTCAGCCAAATGTCAGACCTGTGGCT---CT 717
Qy 985 TCTGTCTTGAAGCGCGAGGAGGCTTCAAGCTTGTGCAAGGTGACCCCTGTGCTCACTT 1044
Db 718 GTGGCTTGTGCGAGAGGTGCAACGCACTCGAAGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 777

Db 1045 CTGTCTTCTACTGAGAGGCCAATGACACCCCAAGCTACTGAGGAGAGAGAGGAGG 1104
Qy 778 GAGACCCCTGAGATATCTGGAGACCCGGGCTTGGCCACCACTTGGGCTGCTCCCAAC 837
Db 1105 GAGACCTCTGAGATATCTGGAGACCCGGGCTTGGCCACCACTGAGGCTGCTCCCAAC 1164
Qy 838 TCAGGCGAGGCGGAG 894
Db 1165 TCAGGCGAGGCGGAG 1224
Qy 895 GAG 954
Db 1225 GAG 1284
Qy 955 GCTTTCAG 1344
Db 1285 ATGTGAG 1404
Qy 1015 CAGGTGCTCTGAG 1464
Db 1345 CAGGTGCTCTGAG 1464
Qy 1075 CAGGTGCTCTGAG 1134
Db 1405 CAGGTGCTCTGAG 1194
Qy 1135 CTTGCTGCTCTGAG 1524
Db 1465 CTTGCTGCTCTGAG 1584
Qy 1195 AAGGTGCTCTGAG 1584
Db 1525 AAGGTGCTCTGAG 1584
Qy 1255 AACCTGCTCTGAG 1314
Db 1585 AACCTGCTCTGAG 1644
Qy 1315 TGCCGCGAG 1344
Db 1645 TGCCGCGAG 1674

RESULT 11
AP366899 6268 bp DNA linear ROD 15-MAY-2001
LOCUS Rattus norvegicus alpha2b-adrenergic receptor (Rng) gene, complete cds.
DEFINITION
ACCESSION AP366899 GI:14039788
VERSION AP366899
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus; Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ORGANISM Rattus.
REFERENCE 1 (bases 1 to 6268)
AUTHORS Schack, S., Cussac, D. and Paris, H.
TITLES Cloning and characterization of the rat alpha2b-adrenergic receptor gene promoter
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6268)
AUTHORS Schack, S., Cussac, D. and Paris, H.
TITLES Direct Submision
JOURNAL Submitted (29-MAR-2001) U388, INSERM, CHU Rangueil, Toulouse 31403, France
FEATURES
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/strain="Sprague-Dawley"
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gene

promoter /gene="Rng"
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/gene="Rng"
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PEPRILPOCELNOAMWITLASISGSPAPCLIMILVYLRIVYIARSHRGGAARGS
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TSRLVATLRGQVLLAKNVGASGQWRRRTOLSRERFTFVLAVIGVAVCWFPFF
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5907..5912
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5989
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BASE COUNT 1234 a 1652 c 1700 g 1680 t 2 others
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Query Match 75.0%; Score 1007.8; DB 10; Length 6268;
Best Local Similarity 84.8%; Pred. No. 1.5e-159; Indels 3; Gaps 1;
Matches 1142; Conservative
Qy 1 ATGAGCACCAAGAGACCCCTACTCCGTCAGAGCCACAGCGCCATACCGCGGCATCACC 60
Db 2795 ATGAGCACCAAGAGACCCCTACTCCGTCAGAGCCACAGCGCCATACCGCGGCATCACC 2854
Qy 61 TTCCTATCTCTTACATCTTGGGCAACCTCGGATCTCTGCTGTGTGACCAAGC 120
Db 2855 TTCCTATCTCTTACATCTTGGGCAACCTCGGATCTCTGCTGTGTGACCAAGC 2914
Qy 121 CGCTGCTGCGCCCTCGAGAACCTGTCGTGTGCTGCGCGCCGCGGCATCTCTG 180
Db 2915 CGCTGCTGCGCCCTCGAGAACCTGTCGTGTGCTGCGCGCCGCGGCATCTCTG 2974
Qy 181 GTGGCAAGCTCATCATCTCTTCTGCTGGCCACAGAGCTGCGCTACTGTACTTC 240
Db 2975 GTGGCAAGCTCATCATCTCTTCTGCTGGCCACAGAGCTGCGCTACTGTACTTC 3034
Qy 241 CGGCGCAGTGTGAGAGTACCTGCGCTGAGCTGCTCTTCTGACCTCTCCATC 300
Db 3035 TGGCGGTGTGTGAGAGTACCTGCGCTGAGCTGCTCTTCTGACCTCTCCATC 3094
Qy 301 GTGACCTGTGTGCGCATCATGCTTGAACCGGCTGAGCGCGCTGAGATC 360
Db 3095 GTGACCTGTGTGCGCATCATGCTTGAACCGGCTGAGCGCGCTGAGATC 3154
Qy 361 AACTCCAAAGGACCGCGCGCATCAAGTGCATCATCTCTGAGCTGAGCTCATCGCC 420
Db 3155 AACTCCAAAGGACCGCGCGCATCAAGTGCATCATCTCTGAGCTGAGCTCATCGCC 480
Qy 421 GCCTCATCTGCTGCGCGCCCTCATCTCAAGAGGCGACAGAGGCGCCAGCGCGGG 3274
Db 3215 GCCTCATCTGCTGCGCGCCCTCATCTCAAGAGGCGACAGAGGCGCCAGCGCGGG 3274
Qy 481 GCCTCATCTGCTGCGCGCCCTCATCTCAAGAGGCGACAGAGGCGCCAGCGCGGG 540

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Db      3275  CTCCCCGAGTGTGAGCTCAACAGAGGCGCTGTGATACATCTTGAGCTCCAGATCGAGTCT 3334
Oy      541   TTCTTTGGCTCGTGGCTCATGATATCTTTGATACCTGGGACCTTACTGATGCCAA 600
Db      3335  TTTTGTCTCCCTGCTCATATGATGCTCTGCTTACCTGGCAATCTTACGTAATGCTCCAA 3394
Oy      601   CGCAGCAACCCGAGAGTCCCAAGGCGGAGGCGGCTGTGGCAGAGGTGATCCAGAG 660
Db      3395  CGCAGCACTGCAAGAGTCTCGAGGCCAAGAGGCGCTGTGGAGAGAGTGAATCCAGAG 3454
Oy      661   CCCCAGCCGACATGTGTGGGCTTTGGGCTTCAAGCAATGCTCCAGCCCTGAGCT--CT 717
Db      3455  CCCCAGCCGAGTGTGGGAGAGTGCACATCTAGTAAAGTGTCCACCTGCTGCTCTCTCT 3514
Oy      718   GTGGCTTCTGCAGAGAGTCAAGGACATCTGAACTGCTGGGAGAGAGAGAGAGAGG 777
Db      3515  CTATCTTCTGTGGAGAGGCCAATGAGACCCCAAGCTTCCAGAGAGAGAGAGAGAGG 3574
Oy      778   GAGACCCCTGAAGATTAAGTGGAGCCGAGGCTTGGCCAGCTTGGGCTGAGCTTCCCA 837
Db      3575  GAGACCCCTGAAGATTAAGTGGAGCCGAGGCTTGGCCAGCTTGGGCTGAGCTTCCCA 3634
Oy      838   TCAGGCGCAGGCGCAGAGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 897
Db      3635  TCAGGCGCAGGCGCAGAGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3694
Oy      898   GAGAGAGAGAGAGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 957
Db      3695  GATAGAGAGAGAGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3754
Oy      958   TGCAGAGCCCGGCTGTGAGCAGCAGCAGAGGAGCTCCGAGGAGTGTGTGTGTGTGT 1017
Db      3755  TGCAGAGCCCGGCTGTGAGCAGCAGCAGGCTTCTGAGGATGAGTGTGTGTGTGTGT 3814
Oy      1018  GTGCTCTGTGAGGAGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1077
Db      3815  GTGCTCTGTGAGGAGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3874
Oy      1078  CTGACCCGAGAGAGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1137
Db      3875  CTGAGCCGAGAGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3934
Oy      1138  TGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1197
Db      3935  TGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3994
Oy      1198  GTGCGCCATGAGCTCTTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1257
Db      3995  GTACCGGATGAGCTCTTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4054
Oy      1258  CTTGTATCTTACCATCTTCAACAGAGCTTCCGCGGTGTGTGTGTGTGTGTGTGTGT 1317
Db      4055  CTTGTATCTTACCATCTTCAACAGAGCTTCCGCGGTGTGTGTGTGTGTGTGTGTGT 4114
Oy      1318  CGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1344
Db      4115  CGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1374

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RESULT 12
AC126878 124474 bp DNA linear HTG 15-NOV-2002
LOCUS Rattus norvegicus clone CH230-263M16, WORKING DRAFT SEQUENCE, 2
DEFINITION
unordered piece.
ACCESSION
AC126878
VERSION
AC126878.4 GI:25007910
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULFILL.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

REFERENCE AUTHORS

1 (bases 1 to 124474)

Muzny, D., Marle, M., Metzger, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alshrooke, S., Amin, A., Angiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaru, M., Barker, M., Barnstead, M., Benham, F., Biewald, K., Blair, J., Blankensbury, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Dreaper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotte, M., Eugene, C., Evans, J., Faller, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C., Gabris, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Georger, G., Georger, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, R., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hulik, S., Hume, J., Idler, D., Jackson, A., Jackson, L., Jacob, L., Jiang, S., Khan, Z., King, L., Kovar, C., Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshuwa, L., Louisedge, H., Lozada, R., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M., McNeill, T., Z., Meenen, E., Miosavljivic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nsokelemeh, O., Okwom, G., Olariunfason, A., Pal, S., Parks, K., Paternak, S., Paul, H., Perez, A., Perez, L., Plambeck, C., Popper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Piazio, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M., A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, R., Riggs, F., Rives, C., Rodkey, T., Rojars, A., Rose, M., Rose, R., Ruiz, S., J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C., D., Smaib, D., Sneed, A., Sodergren, E., Song, X., Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Swatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemami, K., Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, D., Wang, S., Warren, J., Warren, R., Wei, X., White, P., Williams, G., Willson, R., Wleczky, R., Woodden, H., Worley, K., Yu, F., Zhang, J., Zhou, J., Zhou, S., Yen, J., Yoon, L., Yoon, V., Niederhauser, A., Weiss, R., Smith, D., R., Holt, R., A., Smith, H., O., Weinstock, G., and Gibbs, R. A.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 124474)

Direct Submission

Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 124474)

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23907627.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GZCB
Center clone name: CH230-263M16

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 114750 bases at least Q40
Consensus quality: 115674 bases at least Q30
Consensus quality: 116260 bases at least Q20
Estimated insert size: 117568; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 53390: contig of 53390 bp in length
* 53391 53490: gap of unknown length
* 53491 124474: contig of 70984 bp in length.
Location/Qualifiers

FEATURES

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1. 124474

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FEATURES	source
REFERENCE	1 (bases 1 to 2319)
AUTHORS	Zeng,D.W., Harrison,J.K., D'Angelo,D.D., Barber,C.M., Tucker,A.L., Lu,Z.H. and Lynch,K.R.
TITLE	Molecular characterization of a rat alpha-2B-adrenergic receptor
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 87 (8), 3102-3106 (1990)
MEDLINE	90222177
COMMENT	2158103
LOCUS	RAT22BR 2319 bp mRNA linear ROD 27-APR-1993
DEFINITION	Rat alpha-2B-adrenergic receptor (RNG-alpha-2) mRNA, complete cds.
ACCESSION	M32061
VERSION	M32061.1 GI:202589
KEYWORDS	adrenergic receptor.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
FEATURES	1 (bases 1 to 2319)
source	Original source text: Rat (strain Sprague Dawley) adult kidney, cDNA to mRNA, clones dz-3,5,6). Draft entry and computer-readable sequence [1] kindly submitted by K.R.Lynch, 12-FEB-1990. Location/Qualifiers 1..2319

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Job time : 5093.97 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 7, 2004, 18:41:41 ; Search time 393.682 Seconds
(without alignments)
9215.676 Million cell updates/sec

Title: US-09-692-077d-2

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Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues.

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1339.2	99.6	1344	22	AA004761 Human alpha2B-adre
3	1339.2	99.6	1344	24	AA044388 Human alpha-2B-adr
4	1325	98.6	1353	23	AA199905 Human alpha-2BAR t
5	1323.4	98.5	1353	22	AA004762 Human alpha2B-adre
6	1323.4	98.5	1353	24	AA044389 Human alpha-2B-adr
7	1321.8	98.3	2072	25	ACAS6563 Human signalling p
8	1321.8	98.3	3274	25	ABZ42624 Human alpha 2B-adr

9	1302.6	96.9	2064	12	AA014151 Human alpha 2 beta
10	1302.6	96.9	2064	18	AA759499 Human alpha-2b adr
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13	531.6	39.6	6904	24	AB132074 Human immune syste
14	531.6	39.6	6904	24	AA028364 Human chemically t
15	459.4	34.2	1383	23	AA199931 Human alpha-2CAR e
16	459.4	34.2	1383	23	ABZ42625 Human alpha 2c-adr
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18	445.4	33.1	1382	25	ABZ42623 Human alpha 2a-adr
19	445	33.1	1382	15	AA064890 Human derived adre
20	445	33.1	1382	24	ABZ35643 Human gene express
21	445	33.1	1382	25	ACAS6658 Human signalling p
22	444.6	33.1	1371	23	AA199933 Human alpha-2CAR v
23	444.6	33.1	1350	23	AA199917 Human alpha-2BAR e
24	432.6	32.2	3604	25	ACAS6582 Human signalling p
25	304.2	22.6	1758	24	ABZ35339 Human gene express
26	269.8	20.1	4850	24	AA028395 Human chemically t
27	262.6	19.5	1733	24	AB047500 Human chemically t
28	262.6	19.5	1733	24	AB047501 Oligonucleotide fo
29	262.6	19.5	7353	24	AB132073 Human immune syste
30	262.6	19.5	7353	24	AA028363 Human chemically t
31	210.4	15.7	1140	18	AA088392 Corn barnacle G-pr
32	184.8	13.8	3125	23	AB113003 Drosophila melanog
33	184.8	13.8	3335	13	AA021928 Drosophila melanog
34	183.2	13.6	6313	23	AB113002 Oligonucleotide fo
35	181.4	13.5	1733	24	AB047498 Human chemically t
36	181.4	13.5	1733	24	AB047499 Human immune syste
37	181.4	13.5	7353	24	AB132072 Human chemically t
38	181.4	13.5	7353	24	AA028362 Human chemically t
39	171	12.7	1431	18	AA088394 Human amphitrite
40	165.8	12.3	4850	24	AA028394 Human chemically t
41	158.6	11.8	921	15	AA072224 Human alpha-1B adr
42	158.6	11.8	921	16	AA072224 Human alpha-1B adr
43	158.6	11.8	1567	15	AA087879 Human/rat hybrid a
44	158.6	11.8	1567	16	AA087879 Human/rat hybrid a
45	158.6	11.8	1738	15	AA062817 Genomic sequence e

ALIGNMENTS

RESULT 1	AA199906	standard; DNA; 1344 BP.
ID	AA199906	
AC	AA199906;	
XX	XX	
DT	18-FEB-2002	(first entry)
DE	Human alpha-2BAR third intracellular loop variant encoding DNA.	
XX	XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;	
KW	polymorphic site; allelic variant; cardiovascular disease;	
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;	
KW	phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
Key	Location/Qualifiers	
FT	1..1344	
FT	CDS	
FT	/*tag= a	
FT	/product= "alpha-2BAR"	
FT	/note= "sequence is deleted for a 9 nucleotide	
FT	polymorphic site found at nucleotides 901-909	
FT	of the wildtype alpha-2BAR protein (AA199905)"	
PN	WO200179561-A2.	
XX	XX	
PD	25-OCT-2001.	
XX	XX	
PF	17-APR-2001; 2001WO-US12575.	
XX	XX	

17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
(LIGG/) LIGGETT S B.
(SMAL/) SMALL K M.
Liggett SB, Small KM;
WPI: 2001-611728/70.
P-PSDB; AAM52118.
Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
Claim 5; Page 144-145; 163p; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:
(a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A or alpha2C, or fragment or complement of; and
(b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (IIIV) or a site comprising (A) (999GCG99GCG) or (B) (999GCG99GCG) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. ephedrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ABC 239, rauwolfine, idazoxan, tolazoline, phenolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide polymorphic site found at nucleotides 901-909 of the wildtype gene (AA1999905).

Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;

Query Match 100.0%; Score 1344; DB 23; Length 1344;
Best Local Similarity 100.0%; Pred. No. 8.6e-259;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGAGACCAAGAGACCCCTACTCCGTGAGGCAAGAGGCAATAGGAGGAGGATACAC 60
DB 1 ATGAGACCAAGAGACCCCTACTCCGTGAGGCAAGAGGCAATAGGAGGAGGATACAC 60
QY 61 TTCTCATTTCTTTACATCTTGGCAAGCTCTGTGATCTGTGATGTTGACCAAGC 120
DB 61 TTCTCATTTCTTTACATCTTGGCAAGCTCTGTGATCTGTGATGTTGACCAAGC 120
QY 121 CGCTCGTGGCGGCCCTCAGAACCTGTTCTGTGCTGCGCGCGCGCGAGATCTTG 180
DB 121 CGCTCGTGGCGGCCCTCAGAACCTGTTCTGTGCTGCGCGCGCGCGAGATCTTG 180
QY 181 GTGSCAAGCTCATCATCCTTTCTGCTGSCAAGAGGCTGAGGCTATCTGTAATTC 240
DB 181 GTGSCAAGCTCATCATCCTTTCTGCTGSCAAGAGGCTGAGGCTATCTGTAATTC 240
QY 241 CGGCGCAAGTGTGCGAGGTGTACTGCGCTGCAAGCTGCTTCTGACCTGCTCATC 300
DB 241 CGGCGCAAGTGTGCGAGGTGTACTGCGCTGCAAGCTGCTTCTGACCTGCTCATC 300
QY 301 GTGCACTGTGCGCATCAGCTGACCGCTACTGAGCCGTGAGCGCGCTGAGATAC 360
DB 301 GTGCACTGTGCGCATCAGCTGACCGCTACTGAGCCGTGAGCGCGCTGAGATAC 360
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DB 301 GTGCACTGTGCGCATCAGCTGACCGCTACTGAGCCGTGAGCGCGCTGAGATAC 360
QY 361 AACTCCAGAGGACCCCCCGGCGCATCAAGTGAATATCTCTCATCTGTGTGCTCATCGCC 420
DB 361 AACTCCAGAGGACCCCCCGGCGCATCAAGTGAATATCTCTCATCTGTGTGCTCATCGCC 420
QY 421 GCGTCATCTCGTGGCGGCCCTCATCTCAAGAGGAGCAAGAGGAGGAGGAGGAGGAGGAG 480
DB 421 GCGTCATCTCGTGGCGGCCCTCATCTCAAGAGGAGCAAGAGGAGGAGGAGGAGGAGGAG 480
QY 481 CGCCCCAAGTGAAGCTCAACCAAGAGGCGCTGTATCTCTGAGCTTCAGATCGATCTT 540
DB 481 CGCCCCAAGTGAAGCTCAACCAAGAGGCGCTGTATCTCTGAGCTTCAGATCGATCTT 540
QY 541 TTCTTGTCTCTGCTCATCATCATGATCTTGTCTTACTGCGCATCACTGATCGCCAA 600
DB 541 TTCTTGTCTCTGCTCATCATCATGATCTTGTCTTACTGCGCATCACTGATCGCCAA 600
QY 601 CGCAGCAACCGCAGAGGCTCCAGAGGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 601 CGCAGCAACCGCAGAGGCTCCAGAGGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 CCCCGACCGACCATGATGAGGCTTGTGCTCAGCCAACTGCGCAGCTGCTCTGTG 720
DB 661 CCCCGACCGACCATGATGAGGCTTGTGCTCAGCCAACTGCGCAGCTGCTCTGTG 720
QY 721 GCTTCGCAAGAGGTCACAGGACCTGAAAGTCACTGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 721 GCTTCGCAAGAGGTCACAGGACCTGAAAGTCACTGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 ACCCTGAAGATATCTGGAACCGGAGCTTGCACCAAGTGTGAGCTCCCTCCCACTCA 840
DB 781 ACCCTGAAGATATCTGGAACCGGAGCTTGCACCAAGTGTGAGCTCCCTCCCACTCA 840
QY 841 GGCACAGGCGCAAGAGAGGCTGTTTGTGAGGATCTTCAGAGATGAAGTGAAGAGAG 900
DB 841 GGCACAGGCGCAAGAGAGGCTGTTTGTGAGGATCTTCAGAGATGAAGTGAAGAGAG 900
QY 901 GAGGAGAGAGAGAGAGAGTGAACCCAGGAGTCCAGTGTCTCGGCTCAGCTTGC 960
DB 901 GAGGAGAGAGAGAGAGAGTGAACCCAGGAGTCCAGTGTCTCGGCTCAGCTTGC 960
QY 961 AGCCCCCGCTGAGAGGCAAGGAGCTCCGAGTGTGAGGCACTTACGTCGAGGAG 1020
DB 961 AGCCCCCGCTGAGAGGCAAGGAGCTCCGAGTGTGAGGCACTTACGTCGAGGAG 1020
QY 1021 CTCTGAGGAGGAGGAGGCTGTGATGAGTGTGAGGAGTGTGAGGAGGAGGAGGAG 1080
DB 1021 CTCTGAGGAGGAGGAGGCTGTGATGAGTGTGAGGAGTGTGAGGAGGAGGAGGAG 1080
QY 1081 ACCCGGAGAGAGGAGGCTTCACTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1140
DB 1081 ACCCGGAGAGAGGAGGCTTCACTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1140
QY 1141 TGGTTCCTCTTCTTCAAGCTACAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
DB 1141 TGGTTCCTCTTCTTCAAGCTACAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY 1201 CCCCATGAGGCTTTCAGAGTGTCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1260
DB 1201 CCCCATGAGGCTTTCAGAGTGTCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1260
QY 1261 GTTATTAACCATCTTCAACCAAGAGCTTCCGCGGAGCTTCCGAGAGATCTGTGCGCG 1320
DB 1261 GTTATTAACCATCTTCAACCAAGAGCTTCCGCGGAGCTTCCGAGAGATCTGTGCGCG 1320
QY 1321 CCGTGAACCAAGAGGCTGTGA 1344
DB 1321 CCGTGAACCAAGAGGCTGTGA 1344
```

RESULT 2
AAD04761

[illegible]

Db	61	TTCTCATTTCTTTACCATCTTTCGGCAACGCTGCTGTCATCTGAGCTGTGTTCACAGC	120
Qy	121	CGCTGCTGCGCGCCCTCAGAACCTGTGTTCCGTGCTGCTGCGCGCCGCGACATCTCG	180
Db	121	CGCTGCTGCGCGCCCTCAGAACCTGTGTTCCGTGCTGCTGCGCGCCGCGACATCTCG	180
Qy	181	GTGACAGCTCATCATCTCTTCTCGCTGGCCAAAGAGCTGAGGCTACTGATGTAATTC	240
Db	181	GTGACAGCTCATCATCTCTTCTCGCTGGCCAAAGAGCTGAGGCTACTGATGTAATTC	240
Qy	241	CGGCGCAAGTGTGGAGGTGTACTCTGGCGCTCCAGCGTGTCTTCTTGACACTCTGTCATC	300
Db	241	CGGCGCAAGTGTGGAGGTGTACTCTGGCGCTCCAGCGTGTCTTCTTGACACTCTGTCATC	300
Qy	301	GTGACACTGTGGCGCCATCAGCTGTGACCGGCTACTGAGCGCGTGGACGCGCTGAGTAC	360
Db	301	GTGACACTGTGGCGCCATCAGCTGTGACCGGCTACTGAGCGCGTGGACGCGCTGAGTAC	360
Qy	361	AACTTCAGAGCGCACCCCGCGCGCATCAAGTGCATCATCTCACTGTGTGCTCATCGCC	420
Db	361	AACTTCAGAGCGCACCCCGCGCGCATCAAGTGCATCATCTCACTGTGTGCTCATCGCC	420
Qy	421	GCGTCATCTGCTGCGCCCTCATCTTACAGAGGCGACCAAGGCTCCCAAGCGCGCGG	480
Db	421	GCGTCATCTGCTGCGCCCTCATCTTACAGAGGCGACCAAGGCTCCCAAGCGCGCGG	480
Qy	481	CGCCCCAGTGCAGCTCAACAGAGGCGCTGTATCATCTGGGCTCCAGATCGGATCT	540
Db	481	CGCCCCAGTGCAGCTCAACAGAGGCGCTGTATCATCTGGGCTCCAGATCGGATCT	540
Qy	541	TTCTTTGCTCCTTGCCCTCATCATGATCCTTGTCTTACCTGCGCATCTACCTGATCGCAAA	600
Db	541	TTCTTTGCTCCTTGCCCTCATCATGATCCTTGTCTTACCTGCGCATCTACCTGATCGCAAA	600
Qy	601	CGCAGCAACCGCAGAGGTCCTCAGGCGCCAAAGGCGGCGCTGGCGAGGTTGATCCAGCAG	660
Db	601	CGCAGCAACCGCAGAGGTCCTCAGGCGCCAAAGGCGGCGCTGGCGAGGTTGATCCAGCAG	660
Qy	661	CCCCGACCCGACCAATGATGGGGCTTTGGCCTCAGCCAAACTGCGCAGCCCTGGCCTGTG	720
Db	661	CCCCGACCCGACCAATGATGGGGCTTTGGCCTCAGCCAAACTGCGCAGCCCTGGCCTGTG	720
Qy	721	GCTTCTGCGAGAGAGTTCACGGAACCTCGAAGTCCACTGGGAGGAAGAGAGAGGCGAG	780
Db	721	GCTTCTGCGAGAGAGTTCACGGAACCTCGAAGTCCACTGGGAGGAAGAGAGAGGCGAG	780
Qy	781	ACCCTTGAAATCTGGGACCCCGGCGCTTGGCCACCCAGTGGGCTGCGCTTCCCACTCA	840
Db	781	ACCCTTGAAATCTGGGACCCCGGCGCTTGGCCACCCAGTGGGCTGCGCTTCCCACTCA	840
Qy	841	GGCCAGGGGCGAAGAGAGGTTTGTGGGCGCATCTCCAGAGATGAAAGCTGAAAGAGAG	900
Db	841	GGCCAGGGGCGAAGAGAGGTTTGTGGGCGCATCTCCAGAGATGAAAGCTGAAAGAGAG	900
Qy	901	GAGAGAGAGAGAGAGTGTGAACCCCGAGGCAAGTGCATGTCTCGGCGCTCAGCTTGC	960
Db	901	GAGAGAGAGAGAGAGTGTGAACCCCGAGGCAAGTGCATGTCTCGGCGCTCAGCTTGC	960
Qy	961	AGCCCCCGCTGCAGCAGCCACAGGGCTCCCGGGGTCTGGCCACTGACGTGGCCAGGTG	1020
Db	961	AGCCCCCGCTGCAGCAGCCACAGGGCTCCCGGGGTCTGGCCACTGACGTGGCCAGGTG	1020
Qy	1021	CTCTCTGGGCAAGGGCGTGGGTGTATATAGTGGGCAAGTGTGGCGTCCAGAGGCGCAAGTG	1080
Db	1021	CTCTCTGGGCAAGGGCGTGGGTGTATATAGTGGGCAAGTGTGGCGTCCAGAGGCGCAAGTG	1080
Qy	1081	ACCGGAGAGAGCGCTTCACTTGTGTGCTGTGAGTCAATTGAGCGTTTTTGTGTCTCTGC	1140
Db	1081	ACCGGAGAGAGCGCTTCACTTGTGTGCTGTGAGTCAATTGAGCGTTTTTGTGTCTCTGC	1140
Qy	1141	TGGTTCCCTTCTTCTTCAAGTCAAGCTGGGCGCATCTGCGCCGAGACATGCGCAAGTG	1200

Db 1141 TGGTCCCTTCTTCTTACGCTACAGCTGGGGCCATCTGCCCGAAGCATCTGCAAGTG 1200
QY 1201 CCCCATGGCTCTTTCAGATTCTTCTTGTGATCGCTACTGCAAGCATCTGAACCT 1260
Db 1201 CCCCATGGCTCTTTCAGATTCTTCTTGTGATCGCTACTGCAAGCATCTGAACCT 1260
QY 1261 GTTATCTACACATCTTCAACAGAGCTCCGCCGCTTCCGAGAGATCTCTGACCGC 1320
Db 1261 GTTATCTACACATCTTCAACAGAGCTCCGCCGCTTCCGAGAGATCTCTGACCGC 1320
QY 1321 CGGTGACCCAGACGGCTGTGA 1344
Db 1321 CGGTGACCCAGACGGCTGTGA 1344

RESULT 3
AAD44388
ID AAD44388 standard; DNA; 1344 BP.

AC AAD44388;
DT 13-DEC-2002 (first entry)
DE Human alpha-2B-adrenoceptor variant DNA.
XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KW hypertension; hypotensive; variant; gene; de.
XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT CDS 1..1344
FT /*tag= a
FT /product= "Human alpha-2B-adrenoceptor variant
FT protein"

XX WO20026617-A1.

XX 29-AUG-2002.

XX 13-FEB-2002; 2002MO-FI00113.

XX 20-FEB-2001; 2001FI-0000323.

XX (JURI-) JURILAB LTD OY.

XX Salonen J;

XX WPI; 2002-667063/71.

XX P-PSDB; AAB26633.

XX Detecting a risk of hypertension and targeting treatment in a subject
XX by determining the pattern of alleles encoding a variant
XX alpha-2-adrenoceptor -

XX Disclosure; Page 24-26; 35bp; English.

XX The invention relates to a method for detecting a risk of hypertension
XX by determining the pattern of alleles encoding a variant alpha-2B-
XX adrenoceptor (AR) protein. The methods and compositions of the invention
XX are useful for detecting risks and targeting treatment for hypertension.
XX The kit is also useful for selecting for clinical drug trials testing
XX the antihypertensive effect of compounds. The present sequence is human
XX alpha-2B-adrenoceptor variant DNA.

XX Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;

XX Query March 99.64; Score 1339.2; DB 24; Length 1344;

XX Best Local Similarity 99.84; Pred. No. 7.8e-258;

XX Matches 1341; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGCACCAGAGACCCCTACTCCGTGACAGGCCACAGCGGCATTAGCGGCGCATCACC 60

Db 1 ATGAGCACCAGAGACCCCTACTCCGTGACAGGCCACAGCGGCATTAGCGGCGCATCACC 60
QY 61 TTCTCATTTCTTTTACATCTTCCGCAACGCTCTGTATCTCTGCTGTGTGACACG 120
Db 61 TTCTCATTTCTTTTACATCTTCCGCAACGCTCTGTATCTCTGCTGTGTGACACG 120
QY 121 CGCTGCTGCGCCCTCAGAACCTGTTCTGTGTGCTGCTGCGCCCGCCGACATCTTG 180
Db 121 CGCTGCTGCGCCCTCAGAACCTGTTCTGTGTGCTGCTGCGCCCGCCGACATCTTG 180
QY 181 GTGGCAGACGCTATCATCTCTTCTGTGTGCTGCTGCGCCCGCCGACATCTTG 240
Db 181 GTGGCAGACGCTATCATCTCTTCTGTGTGCTGCTGCGCCCGCCGACATCTTG 240
QY 241 CGGCGACAGTGTGCGAGGTATCTGTGCGCTGACGCTGCTCTTCTGCACTGTGATC 300
Db 241 CGGCGACAGTGTGCGAGGTATCTGTGCGCTGACGCTGCTCTTCTGCACTGTGATC 300
QY 301 GTGCACTGTGCGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 360
Db 301 GTGCACTGTGCGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 360
QY 361 AACTCAAGGACACCCCGCGCATCAAGTGCATCACTGCTGCTGCTGCTGCTGCTG 420
Db 361 AACTCAAGGACACCCCGCGCATCAAGTGCATCACTGCTGCTGCTGCTGCTGCTG 420
QY 421 GCGGTATCTGCTGCGCCCTCTCATCAAGGCGACAGGCGCCCGCGCGCGCG 480
Db 421 GCGGTATCTGCTGCGCCCTCTCATCAAGGCGACAGGCGCCCGCGCGCGCGCG 480
QY 481 CGCCCCCATGGAAGTCAACAGAGGCTGTATCTGTGCTGCTGCTGCTGCTGCTG 540
Db 481 CGCCCCCATGGAAGTCAACAGAGGCTGTATCTGTGCTGCTGCTGCTGCTGCTG 540
QY 541 TTCTTGTCTCTTGTGCTCATCATGATCTGTCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TTCTTGTCTCTTGTGCTCATCATGATCTGTCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CGGAGCAACCGAGAGTCCAGAGGCTGCGAGGCGCGCGCGCGCGCGCGCGCG 660
Db 601 CGGAGCAACCGAGAGTCCAGAGGCTGCGAGGCGCGCGCGCGCGCGCGCGCGCG 660
QY 661 CCCGACCGGACATGATGAGGCTTTTGGCTCTGAGCAATGCTGCGCTGCTGCTG 720
Db 661 CCCGACCGGACATGATGAGGCTTTTGGCTCTGAGCAATGCTGCGCTGCTGCTG 720
QY 721 GCTTGTGCAAGAGTCAACGACATCTGAACTCACTGAGGAGAGAGAGAGAG 780
Db 721 GCTTGTGCAAGAGTCAACGACATCTGAACTCACTGAGGAGAGAGAGAGAGAG 780
QY 781 ACCCTGAAAGTATCTGAGACCCCGGCTTGGCACCAGTTGGGCTTCCCACTCA 840
Db 781 ACCCTGAAAGTATCTGAGACCCCGGCTTGGCACCAGTTGGGCTTCCCACTCA 840
QY 841 GGCAGAGGCGAGAGAGAGTGTGTGTGAGGATCTCCAGAGAGTGAAGTGAAGAG 900
Db 841 GGCAGAGGCGAGAGAGAGTGTGTGTGAGGATCTCCAGAGAGTGAAGTGAAGAG 900
QY 901 GAGAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960
Db 901 GAGAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960
QY 961 AGCCCCCGCTGACAGACCAAGAGGCTCCCGGATGTGCGCAACCTTACAGTGA 1020
Db 961 AGCCCCCGCTGACAGACCAAGAGGCTCCCGGATGTGCGCAACCTTACAGTGA 1020
QY 1021 CTCTGTGAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 CTCTGTGAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 ACCCGAGAGAGGCTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

```
Db 1081 ACCGGAGAGAGCGCTTACCTTGTGCTGCTGTGCTATGCGCTTTTGTGCTGTC 1140
Qy 1141 TGGTTCCCTTCTTCTTCACTACAGCTGGGCGCATCTGCGGAGACCTGCAAGATG 1200
Db 1141 TGGTTCCCTTCTTCTTCACTACAGCTGGGCGCATCTGCGGAGACCTGCAAGATG 1200
Qy 1201 CCCCATGAGCTCTTTCAGTTCTTCTTGTGATCGGCTACTGCAACAGCTCACTGACCT 1260
Db 1201 CCCCATGAGCTCTTTCAGTTCTTCTTGTGATCGGCTACTGCAACAGCTCACTGACCT 1260
Qy 1261 GTTATCTACACACATCTTCAACACAGACTCGCGCTGCTTCCGAGAGATCTTGTCCGC 1320
Db 1261 GTTATCTACACACATCTTCAACACAGACTCGCGCTGCTTCCGAGAGATCTTGTCCGC 1320
Qy 1321 CCGTGACCGACGAGCGCTGTGA 1344
Db 1321 CCGTGACCGACGAGCGCTGTGA 1344

RESULT 4
AA199905 standard; DNA, 1353 BP.
ID AA199905;
AC AA199905;
XX
XX 18-FEB-2002 (first entry)
XX
XX Human alpha-2BAR third intracellular loop encoding DNA.
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX polymorphic site; allelic variant; cardiovascular disease;
XX central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX phosphorylation; inositol phosphate; alpha-2BAR;
XX GenBank Accession AF009500; chromosome 2; de.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
XX CDS 1.1353
XX FT /tag= a
XX FT /product= "alpha-2BAR"
XX FT /note= "sequence includes a 9 nucleotide polymorphic site
XX FT at nucleotides 901-909 absent in the alpha-2BAR
XX FT variant. (AA199906)"
XX
XX
XX MO200179561-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001MO-US12575.
XX
XX 17-APR-2000; 2000US-0551744.
XX 10-AUG-2000; 2000US-0636259.
XX 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGSETT S. B.
XX (SMAL/) SMALL K. M.
XX
XX Lligect SB, Small KM;
XX
XX WPI; 2001-611728/70.
XX P-PSDB; AAMS2117.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
XX disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
XX
XX Claim 4; Page 144; 163bp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
```

```
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (gggggggggg) or (B) (gggggggggg) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idazoxan, tolazoline, phenylamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the third intracellular loop of
CC the human alpha-2BAR (GenBank Accession AF009500), the sequence includes
CC a 9 nucleotide polymorphic site at nucleotides 901-909, absent in the
CC alpha-2BAR variant (AA199906).
```

XX SQ Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 other;

XX Query Match 98.6%; Score 1325; DB 23; Length 1353;

XX Best Local Similarity 99.3%; Pred. No. 5.3e-25; Matches 1344; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

```
Qy 1 ATGAGACCAACAGAGACCCCTACTCCGTGACAGGCAACAGCGGCAATAGCGGCGCCATACC 60
Db 1 ATGAGACCAACAGAGACCCCTACTCCGTGACAGGCAACAGCGGCAATAGCGGCGCCATACC 60
Qy 61 TTCTCATTTCTTTTACATCTTGGCAAGCTGTGTCTATCTCTGCTGTGTGACCAAGC 120
Db 61 TTCTCATTTCTTTTACATCTTGGCAAGCTGTGTCTATCTCTGCTGTGTGACCAAGC 120
Qy 121 CGCTCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Db 121 CGCTCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Qy 181 GTGGCAAGCTCATCATCTCTTCTCGCTGGCAACAGAGCTGTGGCTACTGCTATCTTC 240
Db 181 GTGGCAAGCTCATCATCTCTTCTCGCTGGCAACAGAGCTGTGGCTACTGCTATCTTC 240
Qy 241 CGGCGCAAGTGTGCAAGTGTACTGTGCGCTGACGCTGCTCTTCTGCACTGCTGCATC 300
Db 241 CGGCGCAAGTGTGCAAGTGTACTGTGCGCTGACGCTGCTCTTCTGCACTGCTGCATC 300
Qy 301 GTGCACTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 301 GTGCACTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Qy 361 AACTCAAGGAGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 361 AACTCAAGGAGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Qy 421 GCGGTATCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 421 GCGGTATCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Qy 481 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Db 481 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Qy 541 TTCTTGTCTCTGCTCATCATGATCTTGTCTTACTGTGGCATCTACCTGATGCGCAA 600
Db 541 TTCTTGTCTCTGCTCATCATGATCTTGTCTTACTGTGGCATCTACCTGATGCGCAA 600
Qy 601 CGAGCAACCGACGAGGTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 601 CGAGCAACCGACGAGGTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
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QY 661 CCCGACCCGACCATGATGAGGCTTTGAGCTCAAGCCAAATGTCAGCCCTGCGCTGTG 720
Db 661 CCCGACCCGACCATGATGAGGCTTTGAGCTCAAGCCAAATGTCAGCCCTGCGCTGTG 720
QY 721 GCTTCTGCGAGAGAGGTCAACGACATCTGAAATCTCACTGGGAGAAAGAGAGAGAGAG 780
Db 721 GCTTCTGCGAGAGAGGTCAACGACATCTGAAATCTCACTGGGAGAAAGAGAGAGAGAG 780
QY 781 ACCCTGAAGATPACTCTGGGACCCGCGCTTGGCACCCAGTTGGGCTGCCCTTCCCACTCA 840
Db 781 ACCCTGAAGATPACTCTGGGACCCGCGCTTGGCACCCAGTTGGGCTGCCCTTCCCACTCA 840
QY 841 GGGCAGGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 894
Db 841 GGGCAGGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 894
QY 895 ---GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 951
Db 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 952 TCAGCTTGCAGCCCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1011
Db 961 TCAGCTTGCAGCCCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1012 GGGCAGAGTCTCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1071
Db 1021 GGGCAGAGTCTCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1072 GCGCAGCTGACCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1131
Db 1081 GCGCAGCTGACCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1132 GTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
Db 1141 GTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1192 TGCAAGGTGCCCAATGAGCTTCTTCAGTCTTCTTCTGAGATCGGCTACAGCTCA 1251
Db 1201 TGCAAGGTGCCCAATGAGCTTCTTCAGTCTTCTTCTGAGATCGGCTACAGCTCA 1260
QY 1252 CTGAACCTGTTATCTTACATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1311
Db 1261 CTGAACCTGTTATCTTACATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1320
QY 1312 CTGTGCGGCGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1344
Db 1321 CTGTGCGGCGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1353

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RESULT 5
 AAD04762
 ID AAD04762 standard; DNA; 1353 BP.

XX
 AC AAD04762;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
 XX
 KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.

XX
 OS Homo sapiens.
 FH Key
 FT CDS Location/Qualifiers
 FT 1..1353
 FT /tag= a
 FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
 protein"

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PN WC0200129082-A1.
PD 26-APR-2001.
PF 20-OCT-2000; 2000MO-F100913.
PX 22-OCT-1999; 99US-0422985.
XX
XX (JUVA-) JUVANTIA PHARMA LTD OY.
PI Snipit A, Heinoonen P, Alhopuro P, Karonen M, Koulu M, Pesonen U;
PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyysönen K;
PI Salonen R, Kaunonen J, Valkonen V;
DR WPI; 2001-300318/31.
DR P-PSDB; AAB00990.
XX
XX New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular
PT loop of the polypeptide, for treating vascular contraction of coronary
PT arteries -
XX
XX Disclosure; Page 27-29; 37pp; English.
XX
XX The present sequence is a gene encoding human alpha2B-adrenoceptor
CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
CC acids (amino acids 294-311), located in the third intracellular loop of
CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
CC Alpha2-AR mediate many of the physiological effects of the
CC catecholamines, norepinephrine and epinephrine. An antagonist of
CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
CC vascular contraction of coronary arteries and a disease involving
CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
CC clinically expressed as Prinzmetal's variant form or acute myocardial
CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
XX
XX Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;

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Query Match 98.5%; Score 1323.4; DB 22; Length 1353;
 Best Local Similarity 99.3%; Pred. No. 1.1e-254;
 Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

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QY 1 ATGAGCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 1 ATGAGCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 61 TTCCTCATCTCTTACATCTTACATCTTACATCTTACATCTTACATCTTACATCTTACATCT 120
Db 61 TTCCTCATCTCTTACATCTTACATCTTACATCTTACATCTTACATCTTACATCTTACATCT 120
QY 121 CGCTGCTGCGGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 CGCTGCTGCGGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 GTGACAGAGCTATCATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 GTGACAGAGCTATCATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 CGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 CGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 GTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 GTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 AACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 AACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GCGGTATCTGCTGCGGCGCGCTGATCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

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Db 421 GCGCTATCTCGCTGCGCGCCCTCATCTACAGGCGCACAGGCGCCCGCGCGG 480
 Qy 481 CGCCCCAGTGCAGAGCTCAACACAGAGCGCTGTATCCCTGAGCATGATCT 540
 Db 481 CGCCCCAGTGCAGAGCTCAACACAGAGCGCTGTATCCCTGAGCATGATCT 540
 Qy 541 TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTACCTGATGCCAA 600
 Db 541 TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTACCTGATGCCAA 600
 Qy 601 CGCAGCAACCGCAGAGGTCCAGGCGCAAGGCGGCGCTGCGCAGGCTGATCCAGCAG 660
 Db 601 CGCAGCAACCGCAGAGGTCCAGGCGCAAGGCGGCGCTGCGCAGGCTGATCCAGCAG 660
 Qy 661 CCGCGACCGGACATGCTGCGGCGCTTGGCTCAGCCCAACCTGCGCGCTGCTGCTG 720
 Db 661 CCGCGACCGGACATGCTGCGGCGCTTGGCTCAGCCCAACCTGCGCGCTGCTGCTG 720
 Qy 721 GCTTCTGCGCAGAGAGTCAACCGACACTCGAAGTCACTGCGGAGAGAGAGAGAGAG 780
 Db 721 GCTTCTGCGCAGAGAGTCAACCGACACTCGAAGTCACTGCGGAGAGAGAGAGAGAG 780
 Qy 781 ACCCTGTAATATCTGAGAACCCGCGCTTGCACACCACTTGGGCTGCTTCCCACTCA 840
 Db 781 ACCCTGTAATATCTGAGAACCCGCGCTTGCACACCACTTGGGCTGCTTCCCACTCA 840
 Qy 841 GGCAGGCGCGAGAGAGAGGCTTGTGCGGCGCATCTCAAGATGAGTGAAGTGA----- 894
 Db 841 GGCAGGCGCGAGAGAGAGGCTTGTGCGGCGCATCTCAAGATGAGTGAAGTGAAGAGAG 900
 Qy 895 ---GAGAGAGAGAGAGAGAGAGTGAAGCCCGAGGAGTGCAGTGTCTCCGGCC 951
 Db 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGTGAAGCCCGAGGAGTGCAGTGTCTCCGGCC 960
 Qy 952 TCAAGCTTGCAGCGCGCGCTGCGCAGCAGCAGGAGCTCCCGGCTGCGCAGCAGTCACT 1011
 Db 961 TCAAGCTTGCAGCGCGCGCTGCGCAGCAGCAGGAGCTCCCGGCTGCGCAGCAGTCACT 1020
 Qy 1012 GGCAGAGTGTCTCTGCGCAGGCGCTGTGCTGTATAGTGTGCGCAGTGTGCGCTGCAAG 1071
 Db 1021 GGCAGAGTGTCTCTGCGCAGGCGCTGTGCTGTATAGTGTGCGCAGTGTGCGCTGCAAG 1080
 Qy 1072 GGCAGAGTGTCTCTGCGCAGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1131
 Db 1081 GGCAGAGTGTCTCTGCGCAGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1140
 Qy 1132 GTCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1191
 Db 1141 GTCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1200
 Qy 1192 TGCAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1251
 Db 1201 TGCAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1260
 Qy 1252 CTGACCTGTGTATCTATCAACATCTTCAACAGAGACTTCCGCGTGTGCTTCCGAGATC 1311
 Db 1261 CTGACCTGTGTATCTATCAACATCTTCAACAGAGACTTCCGCGTGTGCTTCCGAGATC 1320
 Qy 1312 CTGTGCGCGCGCTGTGAGCCAGAGCGGCTGTGTA 1344
 Db 1321 CTGTGCGCGCGCTGTGAGCCAGAGCGGCTGTGTA 1353

RESULT 6
 AAD4389
 XX AAD4389 standard; DNA; 1353 BP.
 AC AAD4389;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human alpha-2B-adrenoceptor gene.

XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
 KW hypertension; hypotensive; gene; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1353
 FT /*tag= a
 FT /product= "Human alpha-2B-adrenoceptor protein"
 XX
 PN W020026617-A1.
 PD 29-AUG-2002.
 XX
 PF 13-FEB-2002; 2002MO-F100113.
 PR 20-FEB-2001; 2001FI-0000323.
 PA (JURI-) JURILAB LTD OY.
 PI Salonen J.
 XX
 DR WPI; 2002-667063/71.
 DR P-PSDB; AAE26634.
 XX
 PT Detecting a risk of hypertension and targeting treatment in a subject
 PT by determining the pattern of alleles encoding a variant
 FT alpha-2-adrenoceptor
 XX
 PS Disclosure; Page 27-29; 35pp; English.
 XX
 CC The invention relates to a method for detecting a risk of hypertension
 CC by determining the pattern of alleles encoding a variant alpha-2B-
 CC adrenoceptor (AR) protein. The methods and compositions of the invention
 CC are useful for detecting risks and targeting treatment for hypertension.
 CC The kit is also useful for selecting for clinical drug trials testing
 CC the antihypertensive effect of compounds. The present sequence is human
 CC alpha-2B-adrenoceptor gene.
 XX
 SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
 Qy Query Match 98.5%; Score 1323.4; DB 24; Length 1353;
 Db Best Local Similarity 99.3%; Pred. No. 1.1e-254;
 Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;
 Qy 1 ATGAGCACCAAGAGACCCCTTACTCCGTGCAAGGCCAGCGGCATAGCGGCGGCATCACC 60
 Db 1 ATGAGCACCAAGAGACCCCTTACTCCGTGCAAGGCCAGCGGCATAGCGGCGGCATCACC 60
 Qy 61 TTCTCATTTCTTTTACATCTTGGCAACGCTGTGTATCTGCTGTGTGTGACCAAC 120
 Db 61 TTCTCATTTCTTTTACATCTTGGCAACGCTGTGTATCTGCTGTGTGTGACCAAC 120
 Qy 121 CGCTGCTGTGCGCGCCCTGAGACCTGTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180
 Db 121 CGCTGCTGTGCGCGCCCTGAGACCTGTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180
 Qy 181 GTGGCAGCGTATCATTCCTTCTGCTGTGCGCAAGAGCTGTGAGCTTACTGTAATTCT 240
 Db 181 GTGGCAGCGTATCATTCCTTCTGCTGTGCGCAAGAGCTGTGAGCTTACTGTAATTCT 240
 Qy 241 CGGCGCAGTGTGTGCGAGGTGTAAGTGTGCGCTGTGAGCTGTCTTGTGACCTGTGCATC 300
 Db 241 CGGCGCAGTGTGTGCGAGGTGTAAGTGTGCGCTGTGAGCTGTCTTGTGACCTGTGCATC 300
 Qy 301 GTGCACTGTGTGCGCATTCAGCGCTGAGCCGCTACTGTGCGGCGTGAGCGCGCGCTGAGTAC 360
 Db 301 GTGCACTGTGTGCGCATTCAGCGCTGAGCCGCTACTGTGCGGCGTGAGCGCGCGCTGAGTAC 360
 Qy 361 AACTCAGAGGCAACCCCGCGCGCATCAAGTGTGATCATCTCACTGTGTGCTCATTCGCC 420
 Db 361 AACTCAGAGGCAACCCCGCGCGCATCAAGTGTGATCATCTCACTGTGTGCTCATTCGCC 420

OY	421	GGCGTAACTGCGTGGCGGCCCCATATCTACAAAGGCGCACAGAGGCCCCCAGCGCGGG	480
Db	421	GGCGTAACTTGGTGGTGGCGCCCCCTCATCTACAAAGGCGCACAGAGGCCCCCAGCGCGGG	480
OY	481	CGCCCCCAGTGCAGAGCTCAACCAAGAGGCGTGTACATCTCGAGCTCCAGCATCGATCT	540
Db	481	CGCCCCCAGTGCAGAGCTCAACCAAGAGGCGTGTACATCTCGAGCTCCAGCATCGATCT	540
OY	541	TTCTTTGCTCCTTGGCTCATATGATCTTGTCTACCTGCGCATCTACCTGATTCGCCAA	600
Db	541	TTCTTTGCTCCTTGGCTCATATGATCTTGTCTACCTGCGCATCTACCTGATTCGCCAA	600
OY	601	CGAGCAACCGCAGAGGTCGCCAGGGCCAAAGGGGGGGCTTGGCCAGAGGTACCTCAAG	660
Db	601	CGAGCAACCGCAGAGGTCGCCAGGGCCAAAGGGGGGGCTTGGCCAGAGGTACCTCAAG	660
OY	661	CCCCGACCCGACCAATGATGTGGGGCTTTGGCCTCAGGCCAACTGCGCAGCCCTTGCTGTG	720
Db	661	CCCCGACCCGACCAATGATGTGGGGCTTTGGCCTCAGGCCAACTGCGCAGCCCTTGCTGTG	720
OY	721	GCTTCTGCGCAGAGAGGTCAACGGAACCTCGAAATCTACCTGGGGGAAAGAGAGAGGGAG	780
Db	721	GCTTCTGCGCAGAGAGGTCAACGGAACCTCGAAATCTACCTGGGGGAAAGAGAGAGGGAG	780
OY	781	ACCCCTGAAGATACCTGGGACCCGGGCGCTTGGCAACCCAGTTGAGGCTGCGCTTCCCACTCA	840
Db	781	ACCCCTGAAGATACCTGGGACCCGGGCGCTTGGCAACCCAGTTGAGGCTGCGCTTCCCACTCA	840
OY	841	GGCCAGGCGCAGAAAGAGAGGTGTTTGTGGGGCATCTCCAGAGATGAAGTGAAGCTGAA-----	894
Db	841	GGCCAGGCGCAGAAAGAGAGGTGTTTGTGGGGCATCTCCAGAGATGAAGTGAAGAGAG	900
OY	895	---GAGAGAGAGAGAGAGAGAGAAAGTGTGAACCCCAAGGCAAGTGCAGTGTCTCCGGCC	951
Db	901	GAAAGAGAGAGAGAGAGAGAGAAAGTGTGAACCCCAAGGCAAGTGCAGTGTCTCCGGCC	960
OY	952	TCAGCTTGGAGGCCCCCGGTGAGAGCAACAGGCGTCCCGGGTCTGAGCAACCTTACGT	1011
Db	961	TCAGCTTGGAGGCCCCCGGTGAGAGCAACAGGCGTCCCGGGTCTGAGCAACCTTACGT	1020
OY	1012	GGCCAGAGTGCCTCTCGGCGCAGGGGCGTGGGTGTATAGTGGGCACTGGTGGCGTGAAG	1071
Db	1021	GGCCAGAGTGCCTCTCGGCGCAGGGGCGTGGGTGTATAGTGGGCACTGGTGGCGTGAAG	1080
OY	1072	GGCGAGCTGACCCCGGAGAAAGGCTTCACTTCGTGCTGCGTGTGTATATGGGCTTTTT	1131
Db	1081	GGCGAGCTGACCCCGGAGAAAGGCTTCACTTCGTGCTGCGTGTGTATATGGGCTTTTT	1140
OY	1132	GTGCTGTGTTGGTTCGCCCTTCTTCTTCAAGCTACAGCTGGGGGCCATCTGCCCCAAGAC	1193
Db	1141	GTGCTGTGTTGGTTCGCCCTTCTTCTTCAAGCTACAGCTGGGGGCCATCTGCCCCAAGAC	1200
OY	1192	TGCAAGTGCAGCCATGGCTCTTCCAGTTCTTCTTGATCGGCTACTGCAACAGCTCA	1251
Db	1201	TGCAAGTGCAGCCATGGCTCTTCCAGTTCTTCTTGATCGGCTACTGCAACAGCTCA	1260
OY	1252	CTGAACCTCTGTATCTACACCACTTCAACCAAGACTTCCGCGTGCCTTCGAGAGATC	1311
Db	1261	CTGAACCTCTGTATCTACACCACTTCAACCAAGACTTCCGCGTGCCTTCGAGAGATC	1320
OY	1312	CTGTGCGGCGCGTGAACCAAGCGGCTGTGA	1344
Db	1321	CTGTGCGGCGCGTGAACCAAGCGGCTGTGA	1353

RESULT	7
ACAS6583	
ID	ACAS6583 standard; cDNA; 2072 BP
XX	
AC	ACAS6583;
XX	
DT	06-JUN-2003 (first entry)

XX		Human signalling pathway polynucleotide probe SEQ ID NO 1181.
DE		
XX		Human; probe; as; array element; Parkinson's disease;
KW		signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW		immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX		
OS	Homo sapiens.	
PN	US6500938-B1.	
PD	31-DEC-2002.	
PF	30-JAN-1998; 98US-0016434.	
PR	30-JAN-1998; 98US-0016434.	
XX		
PA	(INCY-) INCYTE GENOMICS INC.	
P1	Au-Young J, Seilhamer JJ;	
XX		
DR	WPI; 2003-352189/33.	
XX		
PT	Combination of polynucleotide probes, useful as array elements in a	
PT	microarray for monitoring the expression of a number of target	
PT	polynucleotides -	
PS	Claim 1; SEQ ID NO 1181; 65pp; English.	
XX		
CC	The invention relates to a combination which, comprises a number of	
CC	polynucleotide probes comprising a sequence selected from one of the 1490	
CC	sequences mentioned in the specification. The combination is useful as an	
CC	array element in a microarray for monitoring the expression of a number	
CC	of target polynucleotides. The microarray is particularly useful in the	
CC	diagnosis and treatment of cancer and immunopathology and neuropathology.	
CC	The microarray is useful in diagnostics and treatment regimens, drug	
CC	discovery and development, toxicological and carcinogenicity studies,	
CC	forensics and pharmacogenomics. The microarray is also useful for	
CC	monitoring progression of diseases and for developing sophisticated	
CC	probes for the effects of currently available therapeutic drugs. The	
CC	combination is also useful for purifying a subpopulation of mRNAs, cDNAs	
CC	and genomic fragments and in research and diagnostic applications. The	
CC	array can detect changes in expression in a large number of genes coding	
CC	for different signalling pathway populations which can be used to diagnose	
CC	various diseases including cancer e.g. adenocarcinoma and leukaemia,	
CC	immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease	
CC	and Parkinson's disease. The present sequence represents a polynucleotide	
CC	probe of the invention.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification but was obtained in electronic format directly from USPTO	
CC	at seqdata.uspto.gov/sequence.html?DocID=06500938B1.	
XX		
SQ	Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 other:	
	Query Match 98.3%; Score 1321.8; DB 25; Length 2072;	
	Best Local Similarity 99.2%; Pred. No. 2.4e-25;	
	Matches 1342; Conservative 0; Mismatches 2; Indels 9; Gaps 14;	
OY	1 ATGAGCACACAGAACCCCTACTCGGTGGAGGCCAAGGGGCATGAGGGGCAATACC 60	
DB	413 ATGAGCACACAGAACCCCTACTCGGTGGAGGCCAAGGGGCATGAGGGGCAATACC 472	
OY	61 TTCCTCATTCCTTTTAAACATCTTGCGGACAGCTCTGTATCATCTTGCTGTGTGAACAGC 120	
DB	473 TTCCTCATTCCTTTTAAACATCTTGCGGACAGCTGTGTATCATCTTGCTGTGTGAACAGC 532	
OY	121 GCCTGCTGCGCGCCCCCTGAGAAGCTGTTCTGTGTGTGCTGCGCGCGCGGCAATCCTG 180	
DB	533 CGCTGCTGCGCGCCCCCTGAGAAGCTGTTCTGTGTGTGCTGCGCGCGCGGCAATCCTG 592	
OY	181 GGCGGCAGGCTCATATCATCCCTTTCCGCTGGGCAAGAGGCTGGGCTACTGTAAGTCTTC 240	
OY	593 GTGGGCGAGGCTCATATCATCCCTTTTCGCTGGGCAAGAGGCTGGGCTACTGTAAGTCTTC 652	

QY 241 CCGGCGACGTGTGTCGAGGTGTACCTGCGCTCGACGTGCTTTCTGCACTCTGTCATC 300
Db 653 CCGGCGACGTGTGTCGAGGTGTACCTGCGCTCGACGTGCTTTCTGCACTCTGTCATC 712
QY 301 GTGCACTGTGTGCGCATCAGCTGTGAGCCGCTAGCTGTGAGCCGCGCTGTGAGTAC 360
Db 713 GTGCACTGTGTGCGCATCAGCTGTGAGCCGCTAGCTGTGAGCCGCGCTGTGAGTAC 772
QY 361 AACTCCAAAGGCAACCCCGCGCGCATGAGTCACTCTCACTGTGTGCTCATGACC 420
Db 773 AACTCCAAAGGCAACCCCGCGCGCATGAGTCACTCTCACTGTGTGCTCATGACC 832
QY 421 GCGGTATCTGTGTCGCGCTCTCATCTAACAAGGCGACAGAGGCGCCCAAGCGCGG 480
Db 833 GCGGTATCTGTGTCGCGCTCTCATCTAACAAGGCGACAGAGGCGCCCAAGCGCGG 892
QY 481 CCGCCCCAGTGCAGACTCAACAGAGGCGCTGTATCTGTGCTTCAGCATGAGTCT 540
Db 893 CCGCCCCAGTGCAGACTCAACAGAGGCGCTGTATCTGTGCTTCAGCATGAGTCT 952
QY 541 TTTCTTGTCTGTGCTCTCATCATGATCTGTGTCTACTGTGCGCATCTACCTGATGCGCAA 600
Db 953 TTTCTTGTCTGTGCTCTCATCATGATCTGTGTCTACTGTGCGCATCTACCTGATGCGCAA 1012
QY 601 CCGAGCAACCGCAGAGGTCCAGAGGCGCGCTGTGAGGCGGTGAGTCCAAAGAG 660
Db 1013 CCGAGCAACCGCAGAGGTCCAGAGGCGCGCTGTGAGGCGGTGAGTCCAAAGAG 1072
QY 661 CCGCAGACCGCAGAGGTCCAGAGGCGCGCTGTGAGGCGGTGAGTCCAAAGAG 720
Db 1073 CCGCAGACCGCAGAGGTCCAGAGGCGCGCTGTGAGGCGGTGAGTCCAAAGAG 1132
QY 721 GCTTCTGCGCAGAGGTGCACGACACTCGAAGTCCACTGTGGAGAAAGAGAGGAGGAG 780
Db 1133 GCTTCTGCGCAGAGGTGCACGACACTCGAAGTCCACTGTGGAGAAAGAGAGGAGGAG 1192
QY 781 ACCCTGGAAGATCTGAGGAGCCCGGCGCTGTGAGGCGGTGAGTCCAAAGTCA 840
Db 1193 ACCCTGGAAGATCTGAGGAGCCCGGCGCTGTGAGGCGGTGAGTCCAAAGTCA 1252
QY 841 GCGCAGAGGCGCAGAGAGGAGGTGTGTGTGAGGCACTTCCAGAGTGAAGTGA----- 894
Db 1253 GCGCAGAGGCGCAGAGAGGAGGTGTGTGTGAGGCACTTCCAGAGTGAAGTGAAGAGAG 1312
QY 895 ---GAGAGAGAGAGAGAGAGAGTGAACCCAGCAGTCCAGTGTCTCGGCGC 951
Db 1313 GAGAGAGAGAGAGAGAGAGTGAACCCAGCAGTCCAGTGTCTCGGCGC 1372
QY 952 TCAGCTTTCAGAGCCCGCGCTGACAGCAGCAGGCGCTCCCGGAGTGTGCGCACCTTACCT 1011
Db 1373 TCAGCTTTCAGAGCCCGCGCTGACAGCAGCAGGCGCTCCCGGAGTGTGCGCACCTTACCT 1432
QY 1012 GCGCAGAGTGTCTCTGAGCAGAGGCGCTGTGAGTGAAGTGTGAGTGTGAGTGTGAGG 1071
Db 1433 GCGCAGAGTGTCTCTGAGCAGAGGCGCTGTGAGTGAAGTGTGAGTGTGAGTGTGAGG 1492
QY 1072 GCGCAGAGTGTCTCTGAGCAGAGGCGCTTCACTTGTGTGAGTGTGAGTGTGAGTGTG 1131
Db 1493 GCGCAGAGTGTCTCTGAGCAGAGGCGCTTCACTTGTGTGAGTGTGAGTGTGAGTGTG 1552
QY 1132 GTGCTCTGTGTGTCT 1191
Db 1553 GTGCTCTGTGTGTCT 1612
QY 1192 TGCAAGTGTGCGCATGAGCTCTTCAAGTCTTCTCTGTGAGTGTGAGTGTGAGTGTGAG 1251
Db 1613 TGCAAGTGTGCGCATGAGCTCTTCAAGTCTTCTCTGTGAGTGTGAGTGTGAGTGTGAG 1672
QY 1252 CTGAACCTGTGTATCTTACACCATCTTCAACAGAGTCTTCCGCGTGTCTTCCGAGAGATC 1311
Db 1673 CTGAACCTGTGTATCTTACACCATCTTCAACAGAGTCTTCCGCGTGTCTTCCGAGAGATC 1732

QY 1312 CTGTGCGCGCGGTGAGCCAGACGCGCTGTGA 1344
Db 1733 CTGTGCGCGCGGTGAGCCAGACGCGCTGTGA 1765
RESULT 8
AB242624
ID AB242624 standard; DNA, 3274 BP.
XX
AC AB242624;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US50107.
XX
PR 19-DEC-2000; 2000US-257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.
XX P-PSDB; ABP81780.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
XX
PS Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising:
XX (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular
XX G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity
XX or avidity for a particular GPCR. (1) can be used as GPCR modulators and
XX in gene therapy. The antigenic peptides for GPCRs are useful in detecting
XX an antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be

CC function.
 XX Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
 SQ
 Query Match 96.9%; Score 1302.6; DB 12; Length 2064;
 Best Local Similarity 98.3%; Pred. No. 1.ee-250;
 Matches 1330; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 1 ATGAGCACCAGGAGCCCTACTCCGTGAGAGCCAGAGGCGCATAGGCGGCGCATACC 60
 DB 399 ATGAGCACCAGGAGCCCTACTCCGTGAGAGCCAGAGGCGCATAGGCGGCGCATACC 458
 QY 61 TTCCTATTCTTTTACCATCTTCCGCAAGCTCTGATCATCTGATGATGACAGC 120
 DB 459 TTCCTATTCTTTTACCATCTTCCGCAAGCTCTGATCATCTGATGATGATGACAGC 518
 QY 121 CGCTCGTGGCGCCCTCAAGAACCTTCTGCTGATGCTGCGCCGCGCGCATCTG 180
 DB 519 CGCTCGTGGCGCCCTCAAGAACCTTCTGCTGATGCTGCGCCGCGCGCATCTG 578
 QY 181 GTGAGCAGCTGATCATCTCTTCTGCTGAGAGCCAGAGCTGCTGCTGATCTG 240
 DB 579 GTGAGCAGCTGATCATCTCTTCTGCTGAGAGCCAGAGCTGCTGCTGATCTG 638
 QY 241 CGGCGCAGCTGATGAGAGTGTACTGCGCTGAGAGCTGCTGCTGATCTG 300
 DB 639 CGGCGCAGCTGATGAGAGTGTACTGCGCTGAGAGCTGCTGCTGATCTG 698
 QY 301 GTGAGCAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGTAC 360
 DB 699 GTGAGCAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGTAC 758
 QY 361 AACTCCAGGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGTAC 420
 DB 759 AACTCCAGGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGTAC 818
 QY 421 GCGGTATCTGCTGCGCGCCCTCATCTCAAGAGGAGCCAGAGCCAGAGCCAGAGTAC 480
 DB 819 GCGGTATCTGCTGCGCGCCCTCATCTCAAGAGGAGCCAGAGCCAGAGCCAGAGTAC 878
 QY 481 GCGCCCAAGTGAAGCTCAACAGAGAGCTGTGATCATCTGCTGCTGAGAGTCT 540
 DB 879 GCGCCCAAGTGAAGCTCAACAGAGAGCTGTGATCATCTGCTGCTGAGAGTCT 928
 QY 541 TTCTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 939 TTCTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 998
 QY 601 CGCAGCAACCGCAGAGAGTCCAGAGGAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 DB 999 CGCAGCAACCGCAGAGAGTCCAGAGGAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1058
 QY 661 CCCCGAAGCCGAGAGTGGTGGGCTTTGGCTGAGCCCAAGTGGCAGGCTTGGCTGCTG 720
 DB 1059 CCCCGAAGCCGAGAGTGGTGGGCTTTGGCTGAGCCCAAGTGGCAGGCTTGGCTGCTG 1118
 QY 721 GCTTCTGCGAGAGAGTCAACGAGCACTGCAAGTCTGCTGAGAGAGAGAGAGAGAGAG 780
 DB 1119 GCTTCTGCGAGAGAGTCAACGAGCACTGCAAGTCTGCTGAGAGAGAGAGAGAGAGAG 1178
 QY 781 ACCCTGAGAGTACTGAGGAGCCGAGGCTTGGCAACCCAGTGGGCTGCTTCCCACTCA 840
 DB 1179 ACCCTGAGAGTACTGAGGAGCCGAGGCTTGGCAACCCAGTGGGCTGCTTCCCACTCA 1238
 QY 841 GGGCAGGAGCCAGAGAGGAGTGTGTTGTGAGGCACTTCCAGAGAGTGAAGCTGAA----- 894
 DB 1239 GGGCAGGAGCCAGAGAGGAGTGTGTTGTGAGGCACTTCCAGAGAGTGAAGAGAGAG 1298
 QY 895 ---GAG 951
 DB 1299 GAG 1358
 QY 952 TCAGCTTGAAGCCCGGCTGAGAGAGCCAGAGGAGTCCGAGGAGTGGGCAACCTTACGT 1011

DB 1359 TCAGCTTGAAGCCCGGCTGAGAGAGCCAGAGGAGTCCGAGGAGTGGGCAACCTTACGT 1418
 QY 1012 GGGCAGGAGTCTCTTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1071
 DB 1419 GGGCAGGAGTCTCTTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1478
 QY 1072 GGGCAGGAGTCCGAG 1131
 DB 1479 GGGCAGGAGTCCGAG 1538
 QY 1132 GTGCTGCTGAGTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1191
 DB 1539 GTGCTGCTGAGTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1598
 QY 1192 TGCAGAGTCCAG 1251
 DB 1599 TGCAGAGTCCAG 1658
 QY 1252 CTGAGCCCTGATATCTTCAACCATCTTCAACCATCTTCAACCATCTTCAACCATCTTCAAC 1311
 DB 1659 CTGAGCCCTGATATCTTCAACCATCTTCAACCATCTTCAACCATCTTCAACCATCTTCAAC 1718
 QY 1312 CTGAGCCCTGATATCTTCAACCATCTTCAACCATCTTCAACCATCTTCAACCATCTTCAAC 1344
 DB 1719 CTGAGCCCTGATATCTTCAACCATCTTCAACCATCTTCAACCATCTTCAACCATCTTCAAC 1751

RESULT 10
 AAT59499
 ID AAT59499 standard; DNA; 2064 BP.
 XX
 AC AAT59499;
 DT 25-MAR-2003 (updated)
 DT 06-MAY-1997 (first entry)
 XX
 DE Human alpha-2b adrenergic receptor genomic DNA clone.
 KW Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
 KW epinephrine; signal transduction; neurotransmitter; ligand; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 288..1751
 FT /*tag= a
 XX
 PN US595880-A.
 XX
 PD 21-JUN-1997.
 XX
 PF 22-OCT-1992; 92US-0965040.
 XX
 PR 30-OCT-1989; 89US-0428856.
 PR 30-MAY-1991; 91US-0707604.
 PR 22-OCT-1992; 92US-0965040.
 XX
 PA (SYNA-) SYNAPTIC PHARM CORP.
 XX
 PI Hartig PR, Weinschank RL;
 XX
 DR WPI, 1997-107576/10.
 DR P-PSDB; AAW11804.
 XX
 PT Assay for alpha-2b adrenergic receptor ligands - using membranes of
 PT cells expressing recombinant receptor
 XX
 PS Disclosure, Fig 2A-B; 16pp; English.
 XX
 CC A genomic DNA clone (AAT59499) codes for human alpha-2b adrenergic
 CC receptor (AAW11804), a member of the rhodopsin-like signal transducer
 CC family. It was isolated from a human spleen genomic library in the

